

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 27, 2001, 09:00:04 ; Search time 41.13 seconds

(without alignments)  
208.911 Million cell updates/sec

Title: US-09-889-300a-1

Perfect score: 614

Sequence: 1 QVQLQQSGAELVRPGTSVKV.....ARDGPWFAYWGQGLTVTSA 116

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: /SIDS2/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	614	100.0	116	21	AAB10443	Murine monoclonal
2	554.5	90.3	119	19	AAW49814	Amino acid sequenc
3	554.5	90.3	138	14	AAAR39266	Mouse C4G1 Ig heav
4	554.5	90.3	138	19	AAW49810	Variable region of
5	546.5	89.0	119	18	AAW01580	Lead binding MAb 1
6	515	83.9	137	12	AAAR12360	Heavy chain variab
7	515	83.9	137	12	AAAR12238	Mouse MAB 4D12 H c
8	515	83.9	141	11	AAAR09427	ME4 Heavy Chain V
9	515	83.9	141	18	AAW06216	MAB ME4 heavy chai
10	515	83.9	141	20	AAW85063	Mouse ME4 heavy cha
11	510.5	83.1	138	18	AAW34515	Variable heavy cha

12	503.5	82.0	119	19	AAW49813	Amino acid sequenc
13	503.5	82.0	121	18	AAW07437	Anti-DNA antibody
14	503.5	82.0	222	14	AAAR39267	Humanised C4G1 Ig
15	503.5	82.0	222	19	AAW49817	Fragment of humani
16	503.5	82.0	235	14	AAAR39268	Humanised C4G1 Ig
17	503.5	82.0	235	19	AAW49818	Amino acid sequenc
18	503.5	82.0	449	14	AAAR43339	Completely humanis
19	503.5	82.0	449	19	AAW49816	Amino acid sequenc
20	498.5	81.2	136	8	AAAP70624	Sequence encoded b
21	498.5	81.2	136	18	AAW10584	Anti-hepatitis B h
22	498.5	81.2	136	18	AAW16340	Mouse-human chimae
23	498.5	81.2	136	18	AAW10239	Chimeric anti-hepa
24	498.5	81.2	136	19	AAW47510	Human anti-hepatit
25	498.5	81.2	136	19	AAW41054	Human anti-hepatit
26	498.5	81.2	136	19	AAW47517	Human anti-hepatit
27	498.5	81.2	136	20	AAW89535	Chimeric anti-hepa
28	498.5	81.2	136	22	AAAR8085	Chimeric anti-hepa
29	497.5	81.0	117	17	AAAR8716	Mouse antibody hea
30	492	80.1	272	17	AAW00557	Nematode salivary
31	492	80.1	272	19	AAW43913	Mus musculus antib
32	490.5	79.9	119	18	AAW01585	Lead binding MAB 1
33	490.5	79.9	121	17	AAW00833	Variable heavy cha
34	487.5	79.4	117	14	AAAR35032	GMP-140 MAB heav
35	487.5	79.4	123	21	AAAY78325	Anti-zeta-chain an
36	487.5	79.4	532	21	AAAY78328	Bispecific anti-ze
37	487	79.3	1050	21	AAAB09774	Molecular pathogen
38	485	79.0	114	13	AAAR21273	Murine VH group 1
39	484	78.8	114	13	AAAR21277	Murine VH group 1
40	483	78.7	118	18	AAW27122	Murine antibody he
41	482.5	78.6	119	17	AAW04332	Heavy chain of mon
42	482.5	78.6	121	16	AAW4964	Anti-idiotyp anti
43	482	78.5	114	13	AAAR21281	Murine VH group 1
44	481.5	78.4	119	21	AAAY71473	Mouse monoclonal a
45	481	78.3	121	13	AAAR28806	5A8 VH. Synthetic

#### ALIGNMENTS

RESULT 1  
AAB10443  
ID AAB10443 standard; protein; 116 AA.  
XX  
AC AAB10443;  
XX  
DT 01-DEC-2000 (first entry)  
XX  
DE Murine monoclonal antibody MAK HE2 variable region heavy chain.  
XX  
KW Murine; monoclonal antibody; MAK HE2; heavy chain; variable region;  
KW human cellular membrane antigen; tumor associated antigen; TAA;  
KW vaccine; cancer.  
XX  
OS Mus sp.  
XX  
PN WO200041722-A1.  
XX  
PD 20-JUL-2000.  
XX  
PF 12-JAN-2000; 2000WO-EP00174.  
XX  
PR 13-JAN-1999; 99CH-0000051.  
XX  
PI (IGEN-) IGENEON GMBH.  
XX  
PI Eckert H, Loibner H;  
XX  
DR WPI; 2000-475956/41.  
XX  
PT Novel use of antibodies against human cellular membrane antigens for  
PT vaccination against cancer  
XX  
PS Example 3; Page 47; 54pp; German.

XX This invention describes the novel use of an antibody targeted to a  
 CC human cellular membrane antigen, to manufacture a medicament to  
 CC prophylactically and/or therapeutically vaccinate against cancer.  
 CC The antibodies against tumor associated antigen (TAA) for prophylactic  
 CC and/or therapeutic vaccination against cancer may be used in low doses  
 CC (when compared to antibodies against TAA for passive immunotherapy),  
 CC typically less than 1 mg by injection. The antibodies also have a long  
 CC continual activity that directly induces immunity and their shelf life  
 CC is unlimited (fresh vaccination is always possible). This sequence  
 CC represents the murine monoclonal antibody MAK HE2 variable region heavy  
 CC chain fragment which is used in the method of the invention.  
 XX  
 XX Sequence 116 AA;  
 SQ

Query Match 100.0%; Score 614; DB 21; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-47;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLQSGAEIVRPGTSVKYSCASGYAFNLYLIEWVKRPGQGLEWVINGPGSGGTNY 60  
 Db 1 qvqlqsggaeivrpqtsvkysckasgyafnlyliewvkprpggglewlvngpvgsggtny 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGPWFAYWGQGLTIVTVA 116  
 Db 61 nekfkgtatltdkssstaymqissltsdsavycardgwpfaywgqgltlvtva 116

RESULT 2  
 AAW49814  
 ID AAW49814 standard; Protein; 119 AA.  
 XX  
 AC AAW49814;  
 XX  
 XX 24-SEP-1998 (first entry)  
 XX  
 XX Amino acid sequence of the mouse antibody C4G1 mature heavy chain.  
 XX  
 XX Heavy chain; humanised; immunoglobulin; Ig; mouse C4G1; antibody;  
 XX inhibition; antigen; cardiovascular disease; thromboembolic disorder;  
 XX cancer; acute myocardial infarction; unstable angina; stroke;  
 XX transient ischemic episode; pulmonary embolism; deep vein thrombosis;  
 XX extracorporeal cardiopulmonary circulation.  
 XX  
 XX Mus sp.  
 XX  
 XX Key Location/Qualifiers  
 XX Domain 31..35  
 XX FT /note= "complementarity determining region"  
 XX FT Domain 50..66  
 XX FT /note= "complementarity determining region"  
 XX FT Domain 99..108  
 XX FT /note= "complementarity determining region"  
 XX  
 XX US5777085-A.  
 XX  
 XX 07-JUL-1998.  
 XX  
 XX 17-MAY-1995; 95US-0458516.  
 XX  
 XX 03-MAY-1993; 93US-0059159.  
 XX 20-DEC-1991; 91US-0812111.  
 XX 09-JUN-1992; 92US-0895952.  
 XX 11-SEP-1992; 92US-0944159.  
 XX  
 XX (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 XX Co MS, Tso JY;  
 XX  
 XX WPT; 1998-398136/34.  
 XX  
 XX New humanised immunoglobulin which binds GPIIb/IIIa - derived from

PT mouse C4G1 antibody, used for inhibiting platelet aggregation for  
 PT treating cardiovascular and thromboembolic disorders.  
 XX  
 PS Claim 1; Fig 5B; 35pp; English.  
 XX  
 CC This is the amino acid sequence of the humanised antibody C4G1 heavy  
 CC chain, used in the method of the invention involving the creation  
 CC of a humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody.  
 CC The humanised Ig is capable of binding to GPIIb/IIIa and inhibiting  
 CC platelet aggregation and also the releasing reaction of platelets. The  
 CC Ig can be used for treating cardiovascular diseases and thromboembolic  
 CC disorders, e.g. acute myocardial infarction, unstable angina, stroke,  
 CC transient ischemic episodes, deep vein thrombosis and pulmonary embolism,  
 CC extracorporeal cardiopulmonary circulation. The Ig can also be used in  
 CC diagnosing the presence and location of a thrombus, or certain types of  
 CC cancer cells which develop GPIIb/IIIa on their surfaces, for the  
 CC detection of GPIIb/IIIa antigens or for isolating platelets.  
 XX  
 XX Sequence 119 AA;  
 SQ

Query Match 90.3%; Score 554.5; DB 19; Length 119;  
 Best Local Similarity 91.8%; Pred. No. 4.1e-42;  
 Matches 109; Conservative 3; Mismatches 4; Indels 3; Gaps 2;

QY 1 QVQLQSGAEIVRPGTSVKYSCASGYAFNLYLIEWVKRPGQGLEWVINGPGSGGTNY 60  
 Db 1 qvqlqsggaeivrpqtsvkysckasgyafnlyliewvkprpggglewlvngpvgsggtny 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCA-RDG--PWFAYWGQGLTIVTVA 116  
 Db 61 nekfkgtatltdkssstaymqissltsdsavycardgngwgfaywrgtltvtva 119

RESULT 3  
 AAR39266  
 ID AAR39266 standard; Protein; 138 AA.  
 XX  
 AC AAR39266;  
 XX  
 XX 29-NOV-1993 (first entry)  
 XX  
 XX Mouse C4G1 Ig heavy-chain.  
 XX  
 XX Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIb/IIIa;  
 XX monoclonal antibody; platelet agglutination; humanised antibody.  
 XX  
 XX Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 XX Peptide 1..20  
 XX FT /label= signal\_peptide  
 XX FT Protein 21..138  
 XX FT /label= light\_chain  
 XX FT Region 50..54  
 XX FT /label= complementarity\_determining\_region\_1  
 XX FT Region 69..85  
 XX FT /label= CDR\_2  
 XX FT Region 118..127  
 XX FT /label= CDR\_3  
 XX  
 XX WO9313133-A.  
 XX  
 XX 08-JUL-1993.  
 XX  
 XX 15-DEC-1992; 92WO-JP01630.  
 XX  
 XX 20-DEC-1991; 91US-0812111.  
 XX 09-JUN-1992; 92US-0895952.  
 XX 11-SEP-1992; 92US-0944159.  
 XX  
 XX (PROT-) PROTEIN DESIGN LABS INC.  
 XX  
 XX (YAMA ) YAMANOUCI PHARM CO LTD.







```
Qy 1 QVQLQQSGAEILVRPGTSVKVSKASGYAFTNVLIEWVKRPGQGLEWLVINPGSGGTNY 60
  || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 qvhlqsggaemvrpgtsvkvcragyaftnyllewvkqrpqgglewlgvinpssggtty 79
  ||||| | :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGPWFA--YWGQGTFLVTVA 116
  ||||| | :|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 nekfkdkttmtadkssstaymhlsltsddsavylcartsgghalelywggqgtsvtvss 137
  || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
AAR09427
ID AAR09427 standard; Protein; 141 AA.
XX
AC AAR09427;
XX
DT 04-MAR-1993 (first entry)
XX
DE ME4 Heavy Chain V Region (mouse).
XX
KW Monoclonal antibody; chimera; light; heavy; chain; constant;
KW variable; antigen; diagnosis; cancer; tumour.
XX
OS Mus musculus.
XX
PN WO9002569-A.
XX
PD 22-MAR-1990.
XX
PF 06-SEP-1989; 89WO-US03852.
XX
PR 06-SEP-1988; 88US-0240624.
XX
PR 08-SEP-1988; 88US-0241744.
XX
PR 13-SEP-1988; 88US-0243739.
XX
PR 04-OCT-1988; 88US-0253002.
XX
PR 19-JUN-1989; 89US-0367641.
XX
PR 21-JUL-1989; 89US-0382768.
XX
PA (ITGE-) INT GENETIC ENG INC.
XX
PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
XX
XX WPI; 1990-115825/15.
XX
DR N-PSDB; AAQ08609.
XX
PT Chimeric mouse-human antibodies - prepd. using genes coding for
PT constant human region murine variable region, esp. to 3 tumour
PT antigen
XX
PS Claim 13; Page 123 + Fig 30; 173pp; English.
XX
CC The sequence is used in the prodn. of a chimeric antibody mol.
CC comprising two light chains and two heavy chains, each having a
CC constant region (human) and a variable region (murine) having
CC specificity to an antigen bound by murine monoclonal antibody
CC (Mab) B38.1. The chimeric antibodies can be used for any purpose for
CC which the original murine MAb can be used, with the advantage that
CC they are more compatible with the human body. They are esp. used for
CC the diagnosis and treatment of cancer.
XX
SQ Sequence 141 AA;

Query Match 83.9%; Score 515; DB 11; Length 141;
Best Local Similarity 85.0%; Pred. No. 1.6e-38;
Matches 102; Conservative 4; Mismatches 10; Indels 4; Gaps 2;

Qy 1 QVQLQQSGAEILVRPGTSVKVSKASGYAFTNVLIEWVKRPGQGLEWLVINPGSGGTNY 60
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 qvhlqsggaemvrpgtsvkvcrtsgyaftnyllewvkqrpqgglewlgvinpssgdky 79
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARD--GPWFA--YWGQGTFLVTVA 116
  || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 nekfkdkttmtadkssstaysmqlsltsddsavylfcarghyggyfvmddywggqtsvtvsa 139
  || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

```
Db 80 nenfkkgkatltadkssstaysmqlsltsddsavylfcarghyggyfvmddywggqtsvtvsa 139
  || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9
AAW06216
ID AAW06216 standard; Protein; 141 AA.
XX
AC AAW06216;
XX
DT 13-FEB-1997 (first entry)
XX
DE MAb ME4 heavy chain variable region.
XX
KW Chimeric antigen; monoclonal antibody; ME4: antibody engineering;
KW tumour; antigen; breast carcinoma; colon carcinoma; lung carcinoma;
KW ovary carcinoma; melanoma; cancer; diagnosis; therapy; heavy chain.
XX
OS Mus sp.
XX
PN US5576184-A.
XX
PD 19-NOV-1996.
XX
PF 06-SEP-1988; 88US-0240624.
XX
PR 06-MAY-1991; 91US-0659401.
XX
PR 06-SEP-1988; 88US-0240624.
XX
PR 08-SEP-1988; 88US-0241744.
XX
PR 13-SEP-1988; 88US-0243739.
XX
PR 04-OCT-1988; 88US-0253002.
XX
PR 19-JUN-1989; 89US-0367641.
XX
PR 21-JUL-1989; 89US-0382768.
XX
PR 27-DEC-1994; 94US-0364001.
XX
PA (XOMA ) XOMA CORP.
XX
PI Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;
XX
XX WPI; 1997-011249/01.
XX
DR N-PSDB; AAT43441.
XX
PT Chimeric mouse-human antibodies - recognise a human tumour antigen,
PT used for the treatment and diagnosis of human cancers
XX
PS Example 3; Fig 30; 102pp; English.
XX
CC The heavy chain variable region (AAW06216) of mouse monoclonal
CC antibody ME4 is the product of a cDNA clone (AAT43441) isolated
CC from a ME4 hybridoma cDNA library. Mab ME4 (IgG1) binds to an
CC antigen that is expressed on the surface of human lung, breast,
CC colon and ovary carcinomas and melanomas, but not on most normal
CC adult tissues. The heavy chain and light chain variable regions
CC (see also AAW06215) of ME4 can be linked to human constant regions
CC and expressed in transformed host cells. Novel mouse-human
CC chimeric antibodies (see also AAW06209-14 and AAW06217-18) can be
CC produced that have specificity to human tumour antigens for use in
CC the treatment and diagnosis of human cancer.
XX
SQ Sequence 141 AA;

Query Match 83.9%; Score 515; DB 18; Length 141;
Best Local Similarity 85.0%; Pred. No. 1.6e-38;
Matches 102; Conservative 4; Mismatches 10; Indels 4; Gaps 2;

Qy 1 QVQLQQSGAEILVRPGTSVKVSKASGYAFTNVLIEWVKRPGQGLEWLVINPGSGGTNY 60
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 20 qvhlqsggaemvrpgtsvkvcrtsgyaftnyllewvkqrpqgglewlgvinpssgdky 79
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARD--GPWFA--YWGQGTFLVTVA 116
  || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 nenfkkgkatltadkssstaysmqlsltsddsavylfcarghyggyfvmddywggqtsvtvsa 139
  || |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

## RESULT 10

AAW85063  
ID AAW85063 standard; Protein; 141 AA.

XX AC AAW85063;

XX 16-APR-1999 (first entry)

XX Mouse ME4 heavy chain variable region.

XX Heavy chain variable region; murine antibody ME4; antibody ING-1;  
KW chimeric immunoglobulin; human tumour antigen; chimeric antibody;  
KW treatment; human cancer.

XX OS Mus sp.

XX PN US5843685-A.

XX PD 01-DEC-1998.

XX PF 06-JUN-1995; 95US-0466034.

XX PR 06-SEP-1989; 89WO-US03852.

XX PR 06-SEP-1988; 88US-0240624.

XX PR 08-SEP-1988; 88US-0241744.

XX PR 13-SEP-1988; 88US-0243739.

XX PR 04-OCT-1988; 88US-0253002.

XX PR 19-JUN-1989; 89US-0367641.

XX PR 21-JUL-1989; 89US-0382768.

XX PR 27-DEC-1994; 94US-0364001.

XX PR 06-JUN-1995; 95US-0466034.

XX PA (XOMA ) XOMA CORP.

XX PI Better MD, Chang CP, Horwitz AH, Lei S, Robinson RR;

XX WPI; 1999-044574/04.

XX DR N-PSDB; AAV71159.

XX PT Chimeric antibody specific for human tumour antigen - useful as

XX PT immunoassay, imaging or antitumour agent

XX PS Example 3; Fig 30; 92pp; English.

XX CC The present sequence represents the heavy chain variable region of

XX CC murine antibody ME4. The sequence was used to create chimeric

XX CC mouse-human immunoglobulins which recognise the human tumour

XX CC antigen bound by antibody ING-1 (produced by hybridoma cell line

XX CC ATCC HB 9812). The chimeric antibodies also have an antigen-binding

XX CC site that competitively inhibits the binding of antibody ING-1, and

XX CC mediate complement-dependent cytotoxicity of target cells or

XX CC antibody-dependent cellular cytotoxicity to target cells. The

XX CC chimeric antibodies can be used for therapeutic purposes in the

XX CC treatment of human cancer.

XX SQ Sequence 141 AA;

Query Match 83.9%; Score 515; DB 20; Length 141;  
Best Local Similarity 85.0%; Pred. No. 1.6e-38;  
Matches 102; Conservative 4; Mismatches 10; Indels 4; Gaps 2;

QY 1 QVQLQSGAEIVRPGTSVKVSKKASGYAFNTNLIIEWKORPGGLEWIGVINPGSGGTNY 60

DB 20 qvqlqsgaeivrpqtsvkvscktsctgyafntylmwmkprpgsgglewivinpqsgdaky 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSVAVYFCARD--GPWFA--YWGQGLTVTVA 116

DB 80 nenfkgkatltadksststymqlssltssdsavycfarghyggyfymdywgggtsvtva 139

## RESULT 11

AAW34515

ID AAW34515 standard; Protein; 138 AA.

XX AC AAW34515;

XX DT 19-MAR-1998 (first entry)

XX Variable heavy chain of antibody from hybridoma 5-465-210.

XX Variable region coding sequence; constant region epitope; hybridoma;  
KW antibody detection; antigen/antibody complex; variable heavy chain.

XX OS Mus musculus.

XX PN W09727486-A1.

XX PD 31-JUL-1997.

XX PF 17-JAN-1997; 97WO-US01074.

XX PR 23-JAN-1996; 96US-0589939.

XX PA (ABBO ) ABBOTT LAB.

XX Golden AM, Hackett JR, Hoff JA, Ostrow DH;

XX WPI; 1997-393833/36.

XX DR N-PSDB; AAT98832.

XX PT Use of antibody constant region epitope(s) - as control or  
XX PT calibrator reagents in assays for detecting the presence of an  
XX PT antibody in a test sample

XX PS Disclosure; Page 60; 109pp; English.

XX CC This sequence represents the variable heavy chain of the antibody  
XX CC produced by hybridoma 5-465-210, and can be detected using the method of  
XX CC the invention. The method is for detecting the presence of antibody which  
XX CC may be present in a test sample. It comprises contacting a test sample  
XX CC suspected of containing the antibody with an antigen specific for the  
XX CC antibody to allow the formation of antigen/antibody complexes, detecting  
XX CC the presence of the antibody which may be present in the test sample and  
XX CC employing, as a control or calibrator, a reagent which binds to the  
XX CC antigen. The improvement to this method over previous methods, comprises  
XX CC employing, as the control or calibrator, a reagent comprising one or more  
XX CC antibody constant region epitopes, where the reagent binds to the antigen  
XX CC and is homogeneous with respect to specificity and affinity. The method  
XX CC can be also be used for detecting the presence of antibodies developed  
XX CC against more than one antigen. The method is used particularly for the  
XX CC detection of human antibodies specific for a given antigen, e.g. HIV-1,  
XX CC hepatitis E virus, rubella virus, etc. Use of the reagents circumvent all  
XX CC of the problems associated with using an immune sera in the manufacture  
XX CC of calibrators and positive controls. The present reagents can be readily  
XX CC and reproducibly generated in virtually unlimited quantities and are also  
XX CC useful for quantitating, and monitoring the integrity of, the antigen  
XX CC used in assays.

XX SQ Sequence 138 AA;

Query Match 83.1%; Score 510.5; DB 18; Length 138;  
Best Local Similarity 84.9%; Pred. No. 3.8e-38;  
Matches 101; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQSGAEIVRPGTSVKVSKKASGYAFNTNLIIEWKORPGGLEWIGVINPGSGGTNY 60

DB 20 qvhlqsgaeivrpqtsvkvsckasgyafntyliewtqrpggglewivinpqsgofty 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSVAVYFCAR--DGPWFAYWGQGLTVTVA 116

DB 80 nekfgkatltadksststymqlssltssdsavycartivtdydywgggtpvtvss 138



SQ Sequence 121 AA;  
 Query Match 82.0%; Score 503.5; DB 18; Length 121;  
 Best Local Similarity 82.5%; Pred. No. 1.4e-37;  
 Matches 99; Conservative 3; Mismatches 13; Indels 5; Gaps 1;  
 QY 1 QVQLQSGAELVRPGTSVKVSKKASGYAFNTNYLIEWVKORPGGLEWIGVINPGSGGTNY 60  
 DB 1 qvqlqsgaevkpgssvskvskasgyafntnyliewrqpqggglewlgviyppsggtnt 60  
 QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAYVFCARDG-----PWFAYWGQGLTLVTVS 115  
 DB 1 qvqlqsgaearpgasvklskasgytftsygswvkrtggglewlgviyppsgntyy 60  
 QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAYVFCARDG-----PWFAYWGQGLTLVTVS 115  
 DB 61 nekfgkatltadkssstaymqllssltssdsavycfargysyyswfaywggtlvtvs 120  
 RESULT 14  
 AAR39267  
 ID AAR39267 standard; Protein; 222 AA.  
 AC AAR39267;  
 DT 29-NOV-1993 (first entry)  
 DE Humanised C4G1 Ig heavy-chain Fab fragment.  
 KW Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIa/IIb;  
 KW monoclonal antibody; platelet agglutination; humanised antibody.  
 XX Synthetic.  
 FH Key Location/Qualifiers  
 FT Region 31..35  
 FT Region /label= complementarity\_determining\_region\_1  
 FT Region 50..66  
 FT Region /label= CDR\_2  
 FT Region 99..108  
 FT Region /label= CDR\_3  
 PN W09313133-A.  
 XX 08-JUL-1993.  
 XX 15-DEC-1992; 92WO-JP01630.  
 XX 20-DEC-1991; 91US-0812111.  
 XX 09-JUN-1992; 92US-0895952.  
 XX 11-SEP-1992; 92US-0944159.  
 XX (PROT-) PROTEIN DESIGN LABS INC.  
 XX (YAMA ) YAMANOUCHI PHARM CO LTD.  
 XX Co MS, Tso JY;  
 XX WPI; 1993-227275/28.  
 XX Compasn. contg. immunoglobulin specific for the GP-IIb and -IIIA  
 XX protein - for treating disorders related to vascular thrombosis  
 XX Disclosure; Fig 7C; 54pp; Japanese.  
 XX This is the sequence of the humanised C4G1 immunoglobulin heavy  
 XX chain Fab fragment. See AAR39268 for the F(ab')2 sequence. The  
 XX antibody is specific for the platelet membrane glycoprotein  
 XX GPIIa/IIb and inhibits platelet agglutination. The Ig is thus  
 XX useful in the treatment of thrombosis.  
 XX Sequence 222 AA;  
 Query Match 82.0%; Score 503.5; DB 14; Length 222;  
 Best Local Similarity 80.7%; Pred. No. 2.6e-37;  
 Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

QY 1 QVQLQSGAELVRPGTSVKVSKKASGYAFNTNYLIEWVKORPGGLEWIGVINPGSGGTNY 60  
 DB 1 qvqlqsgaevkpgssvskvskasgyafntnyliewrqpqggglewlgviyppsggtnt 60  
 QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAYVFCAR-DG--PWFAYWGQGLTLVTVA 116  
 DB 61 nekfgkrvtltvdestntaymelsslrtsedavycfarrdngywfaywggtlvtvss 119  
 RESULT 15  
 AAW49817  
 ID AAW49817 standard; Protein; 222 AA.  
 AC AAW49817;  
 DT 24-SEP-1998 (first entry)  
 DE Fragment of humanised antibody C4G1 heavy chain.  
 KW Humanised antibody C4G1; heavy chain; humanised; immunoglobulin; Ig;  
 KW mouse C4G1; antibody; inhibition; antigen; cardiovascular disease;  
 KW thromboembolic disorder; cancer; acute myocardial infarction;  
 KW unstable angina; stroke; transient ischemic episode; pulmonary embolism;  
 KW deep vein thrombosis; extracorporeal cardiopulmonary circulation.  
 XX Chimeric - Mus sp.  
 XX Chimeric - Homo sapiens.  
 PN US5777085-A.  
 XX 07-JUL-1998.  
 XX 17-MAY-1995; 95US-0458516.  
 XX 03-MAY-1993; 93US-0059159.  
 XX 20-DEC-1991; 91US-0812111.  
 XX 09-JUN-1992; 92US-0895952.  
 XX 11-SEP-1992; 92US-0944159.  
 XX (PROT-) PROTEIN DESIGN LABS INC.  
 XX Co MS, Tso JY;  
 XX WPI; 1998-398136/34.  
 XX New humanised immunoglobulin which binds GPIIb/IIIa - derived from  
 XX mouse C4G1 antibody, used for inhibiting platelet aggregation for  
 XX treating cardiovascular and thromboembolic disorders.  
 XX Disclosure; Fig 7C; 35pp; English.  
 XX This is the amino acid sequence of a fragment of humanised antibody  
 XX C4G1 heavy chain, used in the method of the invention involving the  
 XX creation of a humanised immunoglobulin (Ig) derived from the mouse  
 XX C4G1 antibody. The humanised Ig is capable of binding to GPIIb/IIIa  
 XX and inhibiting platelet aggregation and also the releasing reaction of  
 XX platelets. The Ig can be used for treating cardiovascular diseases and  
 XX thromboembolic disorders, e.g. acute myocardial infarction, unstable  
 XX angina, stroke, transient ischemic episodes, deep vein thrombosis and  
 XX pulmonary embolism, extracorporeal cardiopulmonary circulation. The  
 XX Ig can also be used in diagnosing the presence and location of a  
 XX thrombus, or certain types of cancer cells which develop GPIIb/IIIa on  
 XX their surfaces, for the detection of GPIIb/IIIa antigens or for  
 XX isolating platelets.  
 XX Sequence 222 AA;  
 Query Match 82.0%; Score 503.5; DB 19; Length 222;  
 Best Local Similarity 80.7%; Pred. No. 2.6e-37;  
 Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

Qy 1 QVQLQQSGAELVRPCTSVKVSCKASGYAFTNLYLEWVKQRPQGQGLEWIGVINPGSGGTNY 60  
Db 1 qvqlvqsgaevkpgssvkvsckasgyaftnyllewvrqapqgglewlgviypgsggtny 60  
Qy 61 NEKFKGKATLTADKSSSTAYWQLSSTSDSDSAVYFCA-RDG--PWFAFWGOGTLVTVSA 116  
Db 61 nekfkgvrtlvtdestntaymelsslrse dtavfcarrdgnygw faywgqgtlvtvss 119

Search completed: December 27, 2001, 09:01:00  
Job time: 56 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2001, 09:00:04 ; Search time 22.67 seconds  
(without alignments)  
115.147 Million cell updates/sec

Title: US-09-889-300A-1  
Perfect score: 614  
Sequence: 1 QVQLQSGAELVRPGTSVKV.....ARDGPWFAYWGQGLTVTSA 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA: \*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pap: \*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pap: \*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pap: \*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pap: \*  
5: /cgn2\_6/ptodata/2/iaa/PCtUS\_COMB.pap: \*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pap: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554.5	90.3	119	1	US-08-458-516-11
2	554.5	90.3	138	1	US-08-458-516-7
3	546.5	89.0	119	3	US-08-767-128-10
4	510.5	83.1	138	3	US-08-589-939-1
5	503.5	82.0	119	1	US-08-458-516-10
6	503.5	82.0	222	1	US-08-458-516-22
7	503.5	82.0	235	1	US-08-458-516-23
8	503.5	82.0	449	1	US-08-458-516-13
9	497.5	81.0	117	4	US-09-157-370-2
10	490.5	79.9	119	3	US-08-767-128-20
11	485.5	79.1	121	3	US-08-881-037-65
12	485.5	78.6	119	2	US-08-737-560A-10
13	482	78.5	122	2	US-07-916-098A-10
14	480	78.2	137	1	US-08-392-419-2
15	478.5	77.9	123	1	US-08-497-312-15
16	478.5	77.9	123	2	US-08-560-558E-28
17	478	77.9	120	3	US-08-397-411-11
18	478	77.9	122	1	US-08-236-520-9
19	478	77.9	122	5	PCT-US95-05262-9
20	478	77.9	139	2	US-08-656-586-4
21	477	77.7	116	1	US-07-634-278-3
22	477	77.7	116	1	US-07-634-278-14
23	477	77.7	116	1	US-08-477-728-3
24	477	77.7	116	1	US-08-477-728-14
25	477	77.7	116	1	US-08-474-040-3
26	477	77.7	116	1	US-08-474-040-14
27	477	77.7	116	1	US-08-487-200-3

28	477	77.7	116	1	US-08-487-200-14	Sequence 14, Appl
29	477	77.7	116	1	US-08-488-113B-167	Sequence 167, App
30	477	77.7	116	1	US-08-477-484B-167	Sequence 167, App
31	477	77.7	116	1	US-08-107-669D-53	Sequence 53, Appl
32	477	77.7	116	1	US-08-472-788A-85	Sequence 85, Appl
33	477	77.7	116	2	US-08-477-531B-53	Sequence 53, Appl
34	477	77.7	116	2	US-08-646-360-167	Sequence 167, App
35	477	77.7	116	2	US-08-082-842A-85	Sequence 85, Appl
36	477	77.7	116	4	US-08-839-765-167	Sequence 167, App
37	477	77.7	116	4	US-09-136-389-167	Sequence 167, App
38	477	77.7	116	4	US-08-484-537-3	Sequence 3, Appli
39	477	77.7	116	4	US-08-484-537-14	Sequence 14, Appl
40	477	77.7	118	2	US-08-428-257A-74	Sequence 74, Appl
41	477	77.7	118	4	US-07-987-264-14	Sequence 14, Appl
42	477	77.7	239	3	US-08-279-772A-8	Sequence 8, Appli
43	477	77.7	239	4	US-08-902-486-11	Sequence 11, Appl
44	477	77.7	599	1	US-08-463-163-3	Sequence 3, Appli
45	476	77.5	122	3	US-08-767-128-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-08-458-516-11  
; Sequence 11, Application US/08458516  
; Patent No. 5777085  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GPIIB/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/458,516  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/059,159  
; FILING DATE: 03-MAY-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 119 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: N-terminal fragment  
; US-08-458-516-11

Query Match 90.3%; Score 554.5; DB 1; Length 119;  
Best Local Similarity 91.6%; Pred. No. 3.3e-45;  
Matches 109; Conservative 3; Mismatches 4; Indels 3; Gaps 2;





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: Patent No. 6015662
: GENERAL INFORMATION:
: APPLICANT: Hackett, Jr., John R.
: APPLICANT: Hoff, Jane A.
: APPLICANT: Ostrow, David H.
: APPLICANT: Golden, Alan M.
: TITLE OF INVENTION: REAGENTS FOR USE AS CALIBRATORS AND
: TITLE OF INVENTION: CONTROLS
: NUMBER OF SEQUENCES: 70
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Abbott Laboratories
: STREET: 100 Abbott Park Road
: CITY: Abbott Park
: STATE: IL
: COUNTRY: US
: ZIP: 60064-3500
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/589,939
: FILING DATE:
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Becker, Cheryl L.
: REGISTRATION NUMBER: 35,441
: REFERENCE/DOCKET NUMBER: 5865-US.01
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 847-935-1729
: TELEFAX: 847-938-2623
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 138 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PS-08-589-939-1

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: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/458,516
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/059,159
: FILING DATE: 03-MAY-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M.
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 11823-37-3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-326-2400
: TELEFAX: 415-326-2422
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 119 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: FRAGMENT TYPE: N-terminal fragment
: US-08-458-516-10

Query Match 82.0%; Score 503.5; DB 1; Length 119;
Best Local Similarity 80.7%; Pred. No. 2e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps:

Qy 1 QVGLQSGAEFLVPGTISVKVSKASGYAFTNLYLEWVKRPGGLEWIGVINPGSGGTNY 116
Db 1 QVVLVSGAEVKKPGSSVKVSKASGYAFTNLYLEWVRQAPGGGLEWIGVYPCSGGTNY 116
Qy 61 NEKFGKGTATADKSSSTAYMOLSLTSDSSAVFYCA-RDG--PWFAYWGQGLTVTVA 116
Db 61 NEKFGKRVLTLDVSTNTAYMELSLRSEDYAVFYCARRDGNYGWFAYWGQGLTVTVA 119

RESULT 6
US-08-458-516-22
: Sequence 22, Application US/08458516
: Patent No. 5777085
: GENERAL INFORMATION:
: APPLICANT: Co. Man Sung
: APPLICANT: Tso, J. Yun
: TITLE OF INVENTION: Humanized Antibodies Reactive with
: TITLE OF INVENTION: GPIIb/IIIa
: NUMBER OF SEQUENCES: 23
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: William M. Smith
: STREET: One Market Plaza, Steuart Tower, Suite 2000
: CITY: San Francisco
: STATE: California
: COUNTRY: USA
: ZIP: 94105
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/458,516
: FILING DATE:
: CLASSIFICATION: 424
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/059,159
: FILING DATE: 03-MAY-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M.
: REGISTRATION NUMBER: 30,223

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; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-22

Query Match      82.0%; Score 503.5; DB 1; Length 222;
Best Local Similarity 80.7%; Pred. No. 3.9e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

QY 1 QVOLQSGAELVRPGTSVKVSKKASGYAFTNYLIEWVKORPGGLEWIGVINPGSGGTNY 60
   ||| ||||: ||:||||||||||||||||||: ||||||||| ||||||||
Db 1 QVOLQSGAEVKKPGSSVKVSKKASGYAFTNYLIEWVRQAPGGGLEWIGVIYPGSGGTNY 60
   ||| ||||: ||:||||||||||||||||||: ||||||||| ||||||||
QY 61 NEKFKGKATLTADKSSSTAYMOLSSLTSDSAVFCA-RDG--PWFAYWGQGLTVTVA 116
   |||||: ||| ||:||||||| ||| ||:||||||| ||| ||||||||| |||
Db 61 NEKFGRVTLTVDESTNTAYMELLSRSEDYAVYFCARRDGNYGWFAYWGQGLTVTVSS 119
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RESULT 7
US-08-458-516-23
; Sequence 23, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co. Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-23
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Query Match      82.0%; Score 503.5; DB 1; Length 235;
Best Local Similarity 80.7%; Pred. No. 4.1e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

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Db 1 QVOLQSGAEVKKPGSSVKVSKKASGYAFTNYLIEWVRQAPGGGLEWIGVIYPGSGGTNY 60
   ||| ||||: ||:||||||||||||||||||: ||||||||| ||||||||
QY 61 NEKFKGKATLTADKSSSTAYMOLSSLTSDSAVFCA-RDG--PWFAYWGQGLTVTVA 116
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RESULT 8
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co. Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-13

Query Match      82.0%; Score 503.5; DB 1; Length 449;
Best Local Similarity 80.7%; Pred. No. 8.4e-40;
Matches 96; Conservative 12; Mismatches 8; Indels 3; Gaps 2;

QY 1 QVOLQSGAELVRPGTSVKVSKKASGYAFTNYLIEWVKORPGGLEWIGVINPGSGGTNY 60
   ||| ||||: ||:||||||||||||||||||: ||||||||| ||||||||
Db 1 QVOLQSGAEVKKPGSSVKVSKKASGYAFTNYLIEWVRQAPGGGLEWIGVIYPGSGGTNY 60
   ||| ||||: ||:||||||||||||||||||: ||||||||| ||||||||
QY 61 NEKFKGKATLTADKSSSTAYMOLSSLTSDSAVFCA-RDG--PWFAYWGQGLTVTVA 116
   |||||: ||| ||:||||||| ||| ||:||||||| ||| ||||||||| |||
Db 61 NEKFGRVTLTVDESTNTAYMELLSRSEDYAVYFCARRDGNYGWFAYWGQGLTVTVSS 119
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RESULT 9
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US-09-157-370-2
; Sequence 2, Application US/09157370A
; Patent No. 6262238
; GENERAL INFORMATION:
; APPLICANT: STEIPE, Boris
; APPLICANT: STEINBACHER, Stefan
; TITLE OF INVENTION: PROCESS FOR MODIFYING THE STABILITY OF ANTIBODIES
; FILE REFERENCE: P8341-8072
; CURRENT APPLICATION NUMBER: US/09/157.370A
; CURRENT FILING DATE: 1998-09-21
; EARLIER APPLICATION NUMBER: 08/765,179
; EARLIER FILING DATE: 1997-01-14
; EARLIER APPLICATION NUMBER: PCT/EP95/02626
; EARLIER FILING DATE: 1995-07-06
; EARLIER APPLICATION NUMBER: DE/P44 25 115.7
; EARLIER FILING DATE: 1994-07-15
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-157-370-2

Query Match      81.0%; Score 497.5; DB 4; Length 117;
Best Local Similarity 80.3%; Pred. No. 7.1e-40;
Matches 94; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

QY 1 OVQLOQSGAELVRPCTSVKVKCKASGYAFTNYLIEWVKORPQGGLWIGVINPGSGGTNY 60
Db 1 EVQLOQSGGELVKPCASVKLCKASGYFTSYMHVMVKORPCKGLWIGVINPGSGGTNY 60

QY 61 NEKFKGKATLTADKSSSTAYMOLSLTSDSDSAVYFCARDG-PWFAYWGQGLTIVTSA 116
Db 61 NEKFKGKATLTADKSSSTAYMOLSLTSDSDSAVYFCARDG-PWFAYWGQGLTIVTSS 117

RESULT 10
US-08-767-128-20
; Sequence 20, Application US/08767128
; Patent No. 6111079
; GENERAL INFORMATION:
; APPLICANT: WYLIE, DWANE E.
; APPLICANT: LOPEZ, OSVALDO
; APPLICANT: MURRAY, PETER JOSEPH
; APPLICANT: GOEBEL, PETER
; TITLE OF INVENTION: LEAD BINDING POLYPEPTIDES AND
; NUCLEOTIDES CODING THEREFORE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant, Gould, Smith, Edell, Welter & Schmidt
; STREET: 3100 No. 6111079west Center, 90 South Seventh St
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/767,128
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE: 04-DEC-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09258
; FILING DATE: 05-JUN-1996

US-09-157-370-2
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/541,373
; FILING DATE: 10-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/462,798
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Carter, Charles G.
; REGISTRATION NUMBER: 35,093
; REFERENCE/DOCKET NUMBER: 8648.49USFI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/371-5278
; TELEFAX: 612/332-9081
; TELEX:
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
; ORIGINAL SOURCE:
; US-08-767-128-20

Query Match      79.9%; Score 490.5; DB 3; Length 119;
Best Local Similarity 78.2%; Pred. No. 3.3e-39;
Matches 93; Conservative 10; Mismatches 13; Indels 3; Gaps 1;

QY 1 OVQLOQSGAELVRPCTSVKVKCKASGYAFTNYLIEWVKORPQGGLWIGVINPGSGGTNY 60
Db 1 OVQLOQSGVELMKPCASVKICKATGYTFSSYIEWVKORPQGLWIGVEILPGSGGTNY 60

QY 61 NEKFKGKATLTADKSSSTAYMOLSLTSDSDSAVYFCAR---DGPWFAYWGQGLTIVTSA 116
Db 61 NEKFKGKATLTADTSSNTAYMQVSLTSDSDSAVYFCARIYYGHLWFAFYWGQGLTIVTSA 119

RESULT 11
US-08-881-037-65
; Sequence 65, Application US/08881037
; Patent No. 6080588
; GENERAL INFORMATION:
; APPLICANT: Glick, Gary D.
; APPLICANT: Swanson, Patrick C.
; TITLE OF INVENTION: DNA BINDING ANTIBODIES
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/881,037
; FILING DATE: 23-JUN-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/443,540
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Konski, Antoinette F.
; REGISTRATION NUMBER: 34,202
```

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; REFERENCE/DOCKET NUMBER: 203442110710
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX:
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 121 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-881-037-65

Query Match 79.1%; Score 485.5; DB 3; Length 121;
Best Local Similarity 80.0%; Pred. No. 9.7e-39;
Matches 96; Conservative 4; Mismatches 15; Indels 5; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFNLYLIEWYKQRPQGQGLEWIGVINFGSGGTNY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 QVQLLESGAELARPGASVKLSCKASGYFTSYGISWVKQRTGQGLEWIGELYPRSGNTYY 60

QY 61 NEKPKGKATLTADKSSSTAYMQLSSLTSDSNAVYFCARDG-----PWFAYWGQGLTVTVS 115
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NEKPKGKATLTADKSSSTAYMQLSSLTSDSNAVYFCARQSYYSYFWAYWGQGLTVTVS 120

RESULT 12
US-08-737-560A-10
; Sequence 10, Application US/08737560A
; Patent No. 5928893
; GENERAL INFORMATION:
; APPLICANT: KANG, Chang-Yuill
; TITLE OF INVENTION: MONOCLONAL ANTIBODY SPECIFIC FOR HUMAN
; TITLE OF INVENTION: 4-1BB AND CELL LINE PRODUCING SAME
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KANG, Chang-Yuill
; STREET: Professor Apt. Ka-302, #244-2, Bongchun 7-dong,
; STREET: Kwanaak-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 151-057
; ADDRESSEE: KIM, Joong-Gon
; STREET: Hanyang Apt. 72-1213, Apgujung-dong, Kangnam-gu
; CITY: Seoul
; STATE: Seoul
; COUNTRY: Republic of Korea
; ZIP: 135-110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5inch, 1.44MB storage
; COMPUTER: IBM PC/AT
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,560A
; FILING DATE: 13-NOV-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: KR 95-8176
; FILING DATE: 08-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-916-098A-10

; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; OTHER INFORMATION: 4B4-1-1 heavy chain variable region
; US-08-737-560A-10

Query Match 78.6%; Score 482.5; DB 2; Length 119;
Best Local Similarity 79.0%; Pred. No. 1.8e-38;
Matches 94; Conservative 8; Mismatches 14; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFNLYLIEWYKQRPQGQGLEWIGVINFGSGGTNY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 QVQLQPGAELVRPGASVKLSCKASGYTFSSYWMHWYKQRPQGVLEWIGVINFGNGHTNY 60

QY 61 NEKPKGKATLTADKSSSTAYMQLSSLTSDSNAVYFCARD---GPWFAYWGQGLTVTVSA 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NEKPKGKATLTVDKSSSTAYMQLSSLTSDSNAVYFCARSTTARGFAYWGQGLTVTVSA 119

RESULT 13
US-07-916-098A-10
; Sequence 10, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: No. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 122 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-916-098A-10
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 27, 2001, 09:00:04 ; Search time 25.84 seconds  
(without alignments)  
341.960 Million cell updates/sec

Title: US-09-889-300A-1  
Perfect score: 614  
Sequence: 1 QVQLQSGAELVRPGTSVKV.....ARDGPWFAYWGQTLTVTSA 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	535.5	87.2	123	B30560	Ig heavy chain v r
2	526	85.7	123	S60067	Ig heavy chain v r
3	491.5	80.0	119	S20640	Ig heavy chain v r
4	491	80.0	135	A30577	Ig heavy chain pre
5	487.5	79.4	117	JC2269	PL7-6 antibody hea
6	487.5	79.4	119	C30562	Ig heavy chain v r
7	487	79.3	474	G2MS11	Ig gamma-2b chain
8	485	79.0	137	F29380	Ig heavy chain pre
9	484	78.8	118	C30560	Ig heavy chain v r
10	483.5	78.7	118	S38565	Ig heavy chain v r
11	483.5	78.7	138	S21810	Ig heavy chain v r
12	482.5	78.6	246	S38950	Ig gamma chain - m
13	482.5	78.6	446	S40295	Ig gamma-2a chain
14	481.5	78.4	119	E30562	Ig heavy chain v r
15	481	78.3	141	JL0076	Ig heavy chain pre
16	478.5	77.9	119	D30562	Ig heavy chain v r
17	478	77.9	137	E29380	Ig heavy chain pre
18	477.5	77.8	131	A27472	Ig heavy chain pre
19	476	77.5	140	S09216	Ig heavy chain pre
20	475.5	77.4	138	HVMST7	Ig heavy chain pre
21	475	77.4	115	A54378	Ig heavy chain v r
22	473.5	77.1	140	PH1482	Ig heavy chain v r
23	472.5	77.0	118	PL0231	Ig heavy chain v r
24	470	76.5	119	A24672	Ig heavy chain pre
25	469.5	76.5	117	S19966	Ig heavy chain v r
26	469.5	76.5	140	HVMST7	Ig heavy chain pre
27	468	76.2	116	S09962	Ig heavy chain v-D
28	468	76.2	116	S53751	antibody Fab Jel 1
29	467.5	76.1	123	E48677	Ig heavy chain v-D

ALIGNMENTS

RESULT 1  
B30560  
Ig heavy chain V region (28.4.10A) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 23-Jul-1999  
C:Accession: B30560  
R:Matsuda, T.; Kabat, E.A.  
J. Immunol. 142, 863-870, 1989  
A:Title: Variable region cDNA sequences and antigen binding specificity of mouse mono  
A:Reference number: A30560; MUID:89110062  
A:Accession: B30560  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-123 <MAT>  
A:Cross-references: GB:M24369; NID:g195619; PIDN:AAA38373.1; PID:g195620  
C:Superfamily: immunoglobulin V region: immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 87.2%; Score 535.5; DB 2; Length 123;  
Best Local Similarity 87.8%; Pred. No. 1e-41;  
Matches 108; Conservative 1; Mismatches 7; Indels 7; Gaps 2;

Qy 1 QVQLQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60  
Db 1 QVQLQSGAELVRPGTSVKVSCKASGYAFTNYLIEWVKRPGQGLEWIGVINPGSGGTNY 60  
Qy 61 NEKFKGRATLTADKSSSFAYMQLSLSLTSDSSAVYFCAR-----DGPW-FAYWGQGLT 113  
Db 61 NEKFKGRATLTADKSSSFAYMQLSLSLTSDSSAVYFCARSPDYDGYWYFDWAGATT 120  
Qy 114 VSA 116  
Db 121 VSS 123

RESULT 2  
S60067  
Ig heavy chain V region (monoclonal antibody C3, gamma 2A) [validated] - mouse (fragm  
C:Species: Mus musculus (house mouse)  
C:Date: 23-Feb-1996 #sequence\_revision 10-Oct-1997 #text\_change 23-Mar-2001  
C:Accession: S60067  
R:Wien, M.W.; Filman, D.J.; Stura, E.A.; Gulllot, S.; Delpeyroux, F.; Crainic, R.; Ho  
Nat. Struct. Biol. 2, 232-243, 1995  
A:Title: Structure of the complex between the fab fragment of a neutralizing antibody  
A:Reference number: S60066; MUID:95292109  
A:Accession: S60067  
A:Molecule type: mRNA  
A:Residues: 1-123 <WIE>  
A:Cross-references: EMBL:X84698; NID:g773225

R;Wien, M.W.; Hogle, J.M.  
submitted to the Brookhaven Protein Data Bank, January 1995

A:Reference number: A52979; PDB:1FPT

C:Contents: annotation; X-ray crystallography, 3.0 angstroms, residues 1-123

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid

F:15-98/Domain: immunoglobulin homology <IMM>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

F:22-96/disulfide bonds: #status experimental

Query Match 85.7%; Score 526; DB 2; Length 123;  
Best Local Similarity 85.0%; Pred. No. 7.5e-41;  
Matches 102; Conservative 5; Mismatches 9; Indels 4; Gaps 1;

QY 1 QVQLQSGAELVPRGTSVKVSKASGYAFTNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60

Db 1 QVQLQSGAELVPRGTSVKVSKASGYAFTNLYLQIKORPGGLEWIGVINPGSGGTDY 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARD---GPFAYWGQGLTVTVA 116

Db 61 NAFKKGATLTADKSSSIYVQLSSLTSDSAVYFCARDFYDVGDFYWGQGLTVTSS 120

#### RESULT 3

S20640

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999

C:Accession: S20640; S20644

R:Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.

submitted to the EMBL Data Library, February 1992

A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice react

A:Reference number: S20639

A:Accession: S20640

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-119 <LOS>

A:Cross-references: EMBL:X65002; NID:g52600; PIDN:CAA46135.1; PID:g52601; EMBL:X64999; N

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 491.5; DB 2; Length 119;  
Best Local Similarity 77.3%; Pred. No. 9.6e-38;  
Matches 92; Conservative 13; Mismatches 11; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVPRGTSVKVSKASGYAFTNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60

Db 1 EVQLQSGPELVKPGASVKMSCKASGYTFTSYVHWKQKPGRGLEWIGVINPDGSKY 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCAR---DGPWFAYWGQGLTVTVA 116

Db 61 NEMFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARATKGSWFAWYWGQGLTVTVA 119

#### RESULT 4

A30577

Ig heavy chain precursor V region (MRL10) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 04-May-1989 #sequence\_revision 04-May-1989 #text\_change 16-Aug-1996

C:Accession: A30577

R;Kofler, R.; Noonan, D.J.; Levy, D.E.; Wilson, M.C.; Moller, N.P.H.; Dixon, F.J.; Theof

J. Exp. Med. 161, 805-815, 1985

A:title: Genetic elements used for a murine lupus anti-DNA autoantibody are closely rela

A:Reference number: A30577; MUID:85159423

A:Accession: A30577

A:Molecule type: mRNA

A:Residues: 1-135 <KOF>

A:Cross-references: GB:M37621

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 491; DB 2; Length 135;

Best Local Similarity 82.8%; Pred. No. 1.2e-37;

Matches 96; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

QY 1 QVQLQSGAELVPRGTSVKVSKASGYAFTNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60

Db 20 QVQLQSGAELVPRGTSVKVSKASGYAFTNLYLIEWVKORPGGLEWIGVINPGSGSTNY 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGPFAYWGQGLTVTVA 116

Db 80 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARLVGGFAYWGQGLTVTVA 135

#### RESULT 5

JC2269

PL7-6 antibody heavy chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 28-Aug-1985 #sequence\_revision 07-Oct-1994 #text\_change 07-May-1999

C:Accession: JC2269; PC2186

R;Kurume, T.; Katayama, M.; Murakami, K.; Hashino, K.; Kamihagi, K.; Yasumoto, M.; Ka

J. Biochem. 115, 608-614, 1994

A:title: Expression of recombinant mouse/human chimeric antibody specific to human GM

A:Reference number: JC2269; MUID:94334310

A:Accession: JC2269

A:Molecule type: mRNA

A:Residues: 1-117 <KUR>

A:Accession: PC2186

A:Molecule type: protein

A:Residues: 2-27 <KU2>

A:Experimental source: hybridoma cell

C:Comment: this protein is specific to human P-selectin.

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:2-98/Region: V segment

F:15-98/Domain: immunoglobulin homology <IMM>

F:99-106/Region: D segment

F:107-117/Region: J segment

Query Match 79.4%; Score 487.5; DB 2; Length 117;

Best Local Similarity 78.6%; Pred. No. 2.2e-37;

Matches 92; Conservative 10; Mismatches 14; Indels 1; Gaps 1;

QY 1 QVQLQSGAELVPRGTSVKVSKASGYAFTNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60

Db 1 EVQLQSGAELVPRGTSVKVSKASGYTFTSYVHWKQKPGRGLEWIGVINPGTAYTEH 60

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGP-WFAYWGQGLTVTVA 116

Db 61 NOKFKDKATLTADKSSSTAYMQLSSLTSDSAVYFCASGNPAWFAWYWGQGLTVTVA 117

#### RESULT 6

C30562

Ig heavy chain V region (27.7.2) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 16-Aug-1996

C:Accession: C30562

R;Sikder, S.K.; Borden, P.; Gruezo, F.; Akolkar, P.N.; Bhattacharya, S.B.; Morrison,

J. Immunol. 142, 888-893, 1989

A:title: Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen

A:Reference number: A30562; MUID:89110066

A:Accession: C30562

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-119 <SIK>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>





A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-118 <MAT>  
A:Cross-references: GB:M24270; NID:g195615; PIDN:AAA38371.1; PID:g195616  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.8%; Score 484; DB 2; Length 118;  
Best Local Similarity 78.0%; Pred. No. 4.6e-37;  
Matches 92; Conservative 10; Mismatches 14; Indels 2; Gaps 1;

QY 1 QVQLQSGAELVPGTSTSVKSKASGYAFTNTLYIEWVKORPGGLEWIGVINPGSGGTNY 60

DB 1 QVHLQSGAELVPGASVSKASGYTFTSYIHWVKORPGGLEWIGVIDPSNYSYTN 60

QY 61 NEKFKGKATLTADKSSSTAYMOLSSLTSDSAVYFCAR--DGPWFAYWGQGLTVTVSA 116

DB 61 NOKFKKATLTVDKSSNTAYMOLSSLTSDSAVYCARWGTGSWFAYWGQGLTVTVSA 118

#### RESULT 10

S38565  
Ig heavy chain V region (ASW1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

C:Accession: S38565

R:Monestier, M.; Losman, L.J.; Novick, K.E.; Aris, J.P.

submitted to the EMBL Data Library, September 1993

A:Description: Molecular analysis of mercury-induced anti-nucleolar antibodies in H-2s M

A:Reference number: S38559

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-118 <MON>

A:Cross-references: EMBL:X75100; NID:g414157; PIDN:CAA52991.1; PID:g414158

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 483.5; DB 2; Length 118;  
Best Local Similarity 78.8%; Pred. No. 5.1e-37;  
Matches 93; Conservative 9; Mismatches 13; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVPGTSTSVKSKASGYAFTNTLYIEWVKORPGGLEWIGVINPGSGGTNY 60

DB 1 EVQLQSGAELVRAGSVKMSKASGYTFTSYGINWVKORPGGLEWIGYINPGNGYTKY 60

QY 61 NEKFKGKATLTADKSSSTAYMOLSSLTSDSAVYFCARDGP--WFAYWGQGLTVTVS 115

DB 61 NEKFKGKATLTVDKSSSTAYMQLRSLTSDSAVYFCAREGAGSYFDYWGQGLTVTVS 118

#### RESULT 11

S21810  
Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 23-Jul-1999

C:Accession: S21810

R:Ostermeyer, M.; Brack, C.H.; Traunecker, A.; Koehler, G.

submitted to the EMBL Data Library, January 1991

A:Description: Nucleotide sequence of a rearranged VDJ-region of a mouse Ig mu heavy cha

A:Reference number: S21810

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-138 <OST>

A:Cross-references: EMBL:X56936; NID:g54163; PIDN:CAA40257.1; PID:g54164

C:Genetics:

A:Introns: 15/3

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 78.7%; Score 483.5; DB 2; Length 138;  
Best Local Similarity 79.8%; Pred. No. 8e-37;  
Matches 95; Conservative 7; Mismatches 14; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVPGTSTSVKSKASGYAFTNTLYIEWVKORPGGLEWIGVINPGSGGTNY 60

DB 20 QVQLQSGPELVKPGASVSKASGYTFTSYIHWVKORPGGLEWIGIYPGNWNKY 79

QY 61 NEKFKGKATLTADKSSSTAYMOLSSLTSDSAVYFCARD--GPFAYWGQGLTVTVSA 116

DB 80 NEKFKGKATLTADKSSSTAYMOLSSLTSDSAVYFCARNYSSYGLAYWGQGLTVTVSA 138

#### RESULT 12

S38950

Ig gamma chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 19-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Jul-1999

C:Accession: S38950

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;

Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993

A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alp

A:Reference number: S38950; MUID:94128242

A:Accession: S38950

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-246 <KLE>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 78.6%; Score 482.5; DB 2; Length 246;  
Best Local Similarity 79.5%; Pred. No. 1.3e-36;  
Matches 93; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVQLQSGAELVPGTSTSVKSKASGYAFTNTLYIEWVKORPGGLEWIGVINPGSGGTNY 60

DB 1 QIQLQSGPELVKPGASVSKASGYTFTDYIHWVKORPGGLEWIGIYPGSGNTKY 60

QY 61 NEKFKGKATLTADKSSSTAYMOLSSLTSDSAVYFCARDGPW-FAYWGQGLTVTVSA 116

DB 61 NEKFKGKATLTVDTSSTAYMQLSSLTSDSAVYFCARGKFAMDYWGQGSTVTSS 117

#### RESULT 13

S40295

Ig gamma-2a chain (mAb735) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 16-Jul-1999

C:Accession: S40295

R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.;

submitted to the EMBL Data Library, January 1993

A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 again

A:Reference number: S40295

A:Accession: S40295

A:Molecule type: protein

A:Residues: 1-446 <KLE>

C:Genetics:

A:Map position: 12

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid

F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>

F:1-117/Domain: V-D-J region <VDJ>

F:118-446/Domain: C region <CHR>

F:118-214/Domain: C1 region <CH1>

F:215-230/Region: hinge

F:231-340/Domain: C2 region <CH2>

F:341-446/Domain: C3 region <CH3>

F;297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 78.3%; Score 481; DB 2; Length 141;  
Best Local Similarity 77.6%; Pred. NO. 1e-36;  
Matches 90; Conservative 11; Mismatches 15; Indels

[illegible]

Search completed: December 27, 2001, 09:01:39  
Job time: 95 sec

C;Species: Mus musculus (house mouse)  
C;Date: 23-Mar-1989 #sequence\_revision 23-Mar-1989 #text\_change 16-Aug-1996

**A/Title:** Amino acid substitutions in V-H CDR2 change the idiotype but not the antigen-binding site

A; Accession: E30562

A; Molecule type: mRNA

C: Superfamily: immuno

**Keywords:** intellectual disability; self-esteem; self-concept; self-efficacy; self-identity; self-worth; self-esteem; self-concept; self-efficacy; self-identity; self-worth

### Query Match

Matches 93; Conser

Qy 1 QVQLQQSGAELVRN

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JL0076

C: species: Mus musculus

C;Date: 31-Dec-1991 #sec

R; Kaartinen, M.; Rocca-S.

DOI: 10.1002/anie.200500000

A; Reference number: JL00

A; Molecule type: mRNA

A; RESIDUES: I-141 <KAA>  
A: Cross-references: CR:

C; Superfamily: immunoglobulin

F;1-19/Domain: signal seq

F; 20-141/Product: 19 head

F; 50-54/Region: compleme



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2001, 09:00:04 ; Search time 14.63 Seconds  
(without alignments)  
290.712 Million cell updates/sec

Title: US-09-889-300A-1  
Sequence: 1 QVQLQSGAELVRPGTSVKV.....ARDGPWFAYWGQGLTVTVSA 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	475.5	77.4	138	1	HV48_MOUSE
2	471.5	76.8	120	1	HV03_MOUSE
3	469.5	76.5	140	1	HV02_MOUSE
4	466	75.9	139	1	HV07_MOUSE
5	457	74.4	137	1	HV11_MOUSE
6	455.5	74.2	117	1	HV12_MOUSE
7	454.5	74.0	121	1	HV01_MOUSE
8	454.5	74.0	121	1	HV01_MOUSE
9	432	70.4	120	1	HV05_MOUSE
10	429	69.9	117	1	HV04_MOUSE
11	427	69.5	117	1	HV02_MOUSE
12	425	69.2	118	1	HV51_MOUSE
13	414	67.4	117	1	HV06_MOUSE
14	414	67.4	117	1	HV09_MOUSE
15	411	66.9	117	1	HV05_MOUSE
16	411	66.9	117	1	HV49_MOUSE
17	410	66.8	117	1	HV10_MOUSE
18	401.5	65.4	136	1	HV15_MOUSE
19	385	62.7	147	1	HV1C_HUMAN
20	384	62.5	117	1	HV15_MOUSE
21	368	59.9	117	1	HV1G_HUMAN
22	363	59.1	117	1	HV1B_HUMAN
23	356	58.0	114	1	HV00_MOUSE
24	332.5	54.2	117	1	HV1A_HUMAN
25	327	53.3	122	1	HV3G_HUMAN
26	324	52.8	119	1	HV37_MOUSE
27	320	52.1	119	1	HV40_MOUSE
28	316.5	51.5	121	1	HV3J_HUMAN
29	316	51.5	120	1	HV1H_HUMAN
30	314.5	51.2	142	1	HV01_RAT
31	312	50.8	119	1	HV38_MOUSE
32	309.5	50.4	119	1	HV3I_HUMAN
33	308.5	50.2	115	1	HV32_MOUSE

34	308.5	50.2	117	1	HV17_MOUSE	P01786 mus musculu
35	308.5	50.2	117	1	HV41_MOUSE	P01811 mus musculu
36	308.5	50.2	125	1	HV1F_HUMAN	P06326 homo sapien
37	305.5	49.8	117	1	HV42_MOUSE	P01812 mus musculu
38	304.5	49.6	118	1	HV39_MOUSE	P01809 mus musculu
39	303.5	49.4	113	1	HV30_MOUSE	P01799 mus musculu
40	303	49.3	136	1	HV16_MOUSE	P01783 mus musculu
41	301	49.0	126	1	HV3K_HUMAN	P01772 homo sapien
42	300.5	48.9	115	1	HV33_MOUSE	P01802 mus musculu
43	299	48.7	114	1	HV01_CANFA	P01784 canis famil
44	299	48.7	114	1	HV3B_HUMAN	P01763 homo sapien
45	298.5	48.6	113	1	HV27_MOUSE	P01796 mus musculu

ALIGNMENTS

```
RESULT 1
HV48_MOUSE
ID HV48_MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION TEPC 1017 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVNST7.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR SMART; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 127 FRAMEWORK 4.
FT DISULFID 128 138 COMPLEMENTARITY-DETERMINING 3.
FT NON_TER 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;
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Query Match 77.48; Score 475.5; DB 1; Length 138;  
Best Local Similarity 77.3%; Pred. No. 7.5e-42;  
Matches 92; Conservative 8; Mismatches 16; Indels 3; Gaps 2;

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Qy 1 QVQLQSGAELVRPGTSVKVSKASGVAFTNYLLEWKORPGQGLEWIGVNPSSGGTNY 60
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Db 20 QVQLQSGAELVRPGTSVKVSKASGVAFTNYLLEWKORPGQGLEWIGVNPSSGGTNY 79
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Qy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSSAVYFCAR-DG--PWFAYWGQGLTVTVSA 116
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Db 80 NEKFKKATLTVDKSSSTAYMQLSSLTPEEFAYVYCARSDGYDWFVYWGQGLTVTVSA 138
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RESULT 2  
HV03\_MOUSE STANDARD; PRT; 120 AA.  
ID HV03\_MOUSE

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AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idiotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032(1982).
CC -!- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT. JH2.
CC PIR; A02028; HVMSG7.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04E4A167B654AF CRC64;

Query Match 76.8%; Score 471.5; DB 1; Length 120;
Best Local Similarity 76.7%; Pred No. 1.6e-41;
Matches 92; Conservative 8; Mismatches 15; Indels 5; Gaps 1;

QY 2 VOLQSGAELVRPGTSVKVSKCASGYAFTNYLIEWVKQPGGLEWIGVINPGSGGTNYN 61
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 VOLQSGAELVRAGSSVKMSKCRASGYTFTSYGINVWKQPGGLEWIGVINPGNGYTKYN 60

QY 62 EKPKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARD-----GPMFAYWGQGLTVTVA 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 EKPKGKTTLTVDKSSSTAYMQLRSLTSDSAVYFCARSYVYGGSYDFDYWGQGLTVTVA 120

RESULT 3
HV02_MOUSE
ID HV02_MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 93G7 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A/J;
RC MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
RA Capra J.D.;
RT "Somatic mutation in genes for the variable portion of the
RT immunoglobulin heavy chain.";
RL Science 216:309-311(1982).
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
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CC EMBL; J00529; AAA38170.1; -
CC PIR; A02034; MHMS18.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
```

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CC EMBL; J00493; AAA38128.1; -
CC PIR; A02028; HVMSG7.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Antiarsonate antibody; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 25A4CBBE31DA5CE8 CRC64;

Query Match 76.5%; Score 469.5; DB 1; Length 140;
Best Local Similarity 76.9%; Pred No. 3.1e-41;
Matches 93; Conservative 9; Mismatches 14; Indels 5; Gaps 2;

QY 1'QVQLQSGAELVRPGTSVKVSKCASGYAFTNYLIEWVKQPGGLEWIGVINPGSGGTNY 60
   :|||:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|||||:|:|:|
Db 20 EVQLQSGAELVRAGSSVKMSKCRASGYTFTSYGINVWKQPGGLEWIGVINPGNGYNY 79

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARD-----GPMFAYWGQGLTVTVA 115
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 NEKFKGKTTLTVDKSSSTAYMQLRSLTSDSAVYFCARSYVYGGSYDFDYWGQGLTVTVA 139

QY 116 A 116
Db 140 S 140

RESULT 4
HV07_MOUSE
ID HV07_MOUSE STANDARD; PRT; 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION B1-8/186-2 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RC MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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-----
CC EMBL; J00529; AAA38170.1; -
CC PIR; A02034; MHMS18.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
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FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FD0C9F465 CRC64;

Query Match
Best Local Similarity 74.28; Score 466; DB 1; Length 139;
Matches 89; Conservative 11; Mismatches 16; Indels 4; Gaps 1;

Qy 1 QVQLQSGAEILVRPGTSVKVSKASGYAFTNYLIWVKRPGQGLEWIGVINPQSGGNTY 60
Db 20 QVQLQSGAEILVKPGASVKLSCKASGYFTSYMHVWVQKRPGRGLEWIGRIDPNSGGTKY 79
Qy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSDSAVYFCAR----DGPWFAYWGQGLTVTVSA 116
Db 80 NEKFKSKATLTVDKPSSTAYMQLSLTSDSDSAVYCYARYDYGGSYFDYWGQGLTLTVSS 139

RESULT 5
HV11_MOUSE
ID HV11_MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION S43 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NpB family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC ENBL: J00539; AAA38172.1; -.
DR PIR; A02038; G2MS43.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 FRAMEWORK 3.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
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FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match
Best Local Similarity 74.4%; Score 457; DB 1; Length 137;
Matches 87; Conservative 12; Mismatches 17; Indels 2; Gaps 1;

Qy 1 QVQLQSGAEILVRPGTSVKVSKASGYAFTNYLIWVKRPGQGLEWIGVINPQSGGNTY 60
Db 20 QVQLQSGAEILVKPGASVKLSCKASGYFTSYLMHVVNQKRPGRGLEWIGRIDPNSGGTTY 79
Qy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSDSAVYFCARD--GPWFAYWGQGLTVTVSA 116
Db 80 NEHFRSKATLTIDKPSSTAYMQLSLTSDSDSAVYCYARYRLGRYFDYWGQGLTLTVSS 137

RESULT 6
HV12_MOUSE
ID HV12_MOUSE STANDARD; PRT; 117 AA.
AC P01756;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOPC 104E.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83075344; PubMed=6816276;
RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
RA Hood L.E.;
RT "Complete amino acid sequence of a mouse mu chain: homology among
RT heavy chain constant region domains.";
RL Biochemistry 21:5415-5424(1982).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
CC PROTEIN HAS ALSO BEEN DETERMINED.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A02039; MHMS4E.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR Immunoglobulin V region; Glycoprotein.
FT DISULFID 22 96 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .).
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;

Query Match
Best Local Similarity 73.5%; Score 455.5; DB 1; Length 117;
Matches 86; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

Qy 1 QVQLQSGAEILVRPGTSVKVSKASGYAFTNYLIWVKRPGQGLEWIGVINPQSGGNTY 60
Db 1 EVQLQSGPELVKPGASVKMSCKASGYFTTDYKMKWKQSHGKSLIEWIGDINPNNGGTSY 60
Qy 61 NEKFKGKATLTADKSSSTAYMQLSLTSDSDSAVYFCARDGPW-FAYWGQGLTVTVSA 116
Db 61 NQKFKGKATLTVDKSSSTAYMQLSLTSDSDSAVYCYARYDYFDYWGAGTTVTVSS 117

RESULT 7
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
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DE IG HEAVY CHAIN V REGION J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevinger B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -1- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -1- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
DR PIR; A26242; MHMSJ5.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DISULFID 22 96
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447B41 CRC64;

Query Match 74.0%; Score 454.5; DB 1; Length 117;
Best Local Similarity 73.5%; Pred. No. 8.8e-40;
Matches 86; Conservative 14; Mismatches 16; Indels 1; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFNYLIEWVKRPGOGLEWIGVNPISGGTNY 60
Db :||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 EVQLQSGELVPGASVKSCASGYFTFDYWKVKVQSHGSLWIGDINPNGGTSY 60

QY 61 NEKFKGKATLADKSSSTAYMQLSSLTSDSAYVFCAR----DGPWFAYWGQGLTVTVA 116
Db :||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 NQKFKGKATLTVDKSSSTAYMQLNSLTSDSAYVVCARDRYWYFDVWGAGTTVTSS 117

RESULT 8
HV01_MOUSE
ID HV01_MOUSE STANDARD; PRT; 121 AA.
AC P01745;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MPC 11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81053741; PubMed=6253904;
RA Zakut R., Cohen J., Givol D.;
RT "Cloning and sequence of the cDNA corresponding to the variable
RT region of immunoglobulin heavy chain MPC11.";
RL Nucleic Acids Res. 8:3591-3601(1980).
RN [2]
RP REVISIONS.
RA Zakut R., Cohen J., Givol D.;
RL Nucleic Acids Res. 8:4839-4840(1980).
CC -1- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED
CC FROM A MYELOMA THAT SECRETES IGG2B.
DR PIR; A02027; GWSM11.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

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Query Match 74.0%; Score 454.5; DB 1; Length 121;
Best Local Similarity 71.9%; Pred. No. 9.1e-40;
Matches 87; Conservative 11; Mismatches 18; Indels 5; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFNYLIEWVKRPGOGLEWIGVNPISGGTNY 60
Db :||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 EAQLQSGAELVRPGTSVKISCAAGYFTFNYIGWKRPKHGLEWIGDIYPGGGFTNY 60

QY 61 NEKFKGKATLADKSSSTAYMQLSSLTSDSAYVFCAR----DGPWFAYWGQGLTVTVA 115
Db :||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 NDNLKGAATLADTSSSTAYIQLSSLTSDSAYVHCARGIYVNSSPYFDSWGQGTITVS 120

QY 116 A 116
Db 121 S 121

RESULT 9
HV50_MOUSE
ID HV50_MOUSE STANDARD; PRT; 120 AA.
AC P06329;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02037; MHMS15.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98
FT DOMAIN 99 105
FT DOMAIN 106 120
FT DISULFID 22 96
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453F426F09834 CRC64;

Query Match 70.4%; Score 432; DB 1; Length 120;
Best Local Similarity 69.2%; Pred. No. 1.8e-37;
Matches 83; Conservative 13; Mismatches 20; Indels 4; Gaps 2;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFNYLIEWVKRPGOGLEWIGVNPISGGTNY 60
Db :||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 QVQLQPGTELVRPGASVNLSCASGYFTFSYWHWIRQRPQOGLEWIGINPSNGGTNY 60

QY 61 NEKFKGKATLADKSSSTAYMQLSSLTSDSAYVFCAR---DGP-WFAYWGQGLTVTVA 116
Db :||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
1 NEKFKGKATLTVDKSSSATYMQLSLTPTSDSAYVVCARDYEDGRYFDVWGTTVTVA 120

RESULT 10
HV04_MOUSE
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 23 PRECURSOR.

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OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE=81234548; PubMed=6788376;  
 RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,  
 RA Baltimore D.;  
 RT "Heavy chain variable region contribution to the NPb family of  
 RT antibodies: somatic mutation evident in a gamma 2a variable region.";  
 RL Cell 24:625-637(1981).  
 CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY  
 CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.  
 DR PIR: A02030; HVMS23.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig: 1.  
 DR SMART; SM00406; Igv: 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.  
 FT DOMAIN 20 49 FRAMEWORK 1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 59 85 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 86 117 FRAMEWORK 3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 69.9%; Score 429; DB 1; Length 117;  
 Best Local Similarity 81.6%; Pred. No. 3.5e-37;  
 Matches 80; Conservative 7; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 QVQLQSGAEIVRPGTSVKVCKASGYAFTNYLIEWVKORPGQGLEWIGVINPGSGGTNY 60  
 DB 20 QVQLQPGTELKPKASVKLSCKASGYFTSYWVHWVKORPGQGLEWIGNINPGNGGTNY 79  
 QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSVAVFPCAR 98  
 DB 80 NEKFKSKVTLTVDKSSSTAYTQLSSLTSDSVAVFPCAR 117  
 RESULT 11  
 HV52\_MOUSE STANDARD; PRT: 117 AA.  
 AC P06327;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION VH558 A1/A4 PRECURSOR.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85099340; PubMed=2578321;  
 RA Yancopoulos G.D., Alt F.W.;  
 RA "Developmentally controlled and tissue-specific expression of  
 RT unrearranged VH gene segments.";  
 RL Cell 40:271-281(1985).

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CC EMBL; M13787; AAA38499.1; -  
 DR PIR: A02029; HVMSA1.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig: 1.  
 DR SMART; SM00406; Igv: 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.  
 FT DOMAIN 20 49 FRAMEWORK 1.  
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.  
 FT DOMAIN 55 68 FRAMEWORK 2.  
 FT DOMAIN 59 85 COMPLEMENTARITY-DETERMINING 2.  
 FT DOMAIN 86 117 FRAMEWORK 3.  
 FT DISULFID 41 115 BY SIMILARITY.  
 FT NON\_TER 117 117  
 SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 69.5%; Score 427; DB 1; Length 117;  
 Best Local Similarity 83.7%; Pred. No. 5.7e-37;  
 Matches 82; Conservative 5; Mismatches 11; Indels 0; Gaps 0;  
 QY 1 QVQLQSGAEIVRPGTSVKVCKASGYAFTNYLIEWVKORPGQGLEWIGVINPGSGGTNY 60  
 DB 20 QVQLQSGPELVKPKALVKISCKASGYFTSYDINWVKORPGQGLEWIGWIYPGDGSTKY 79  
 QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSVAVFPCAR 98  
 DB 80 NEKFKGKATLTADKSSSTAYMQLSSLTSENSAVVFPCAR 117

RESULT 12  
 HV51\_MOUSE STANDARD; PRT: 118 AA.  
 AC P06330;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG HEAVY CHAIN V REGION AC38 205.12.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=84182519; PubMed=6201362;  
 RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;  
 RT "A V region determinant (idiotope) expressed at high frequency in B  
 RT lymphocytes is encoded by a large set of antibody structural genes";  
 RL EMBO J. 3:517-523(1984).  
 DR PIR: A02040; MHMS38.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_v.  
 DR Pfam; PF00047; Ig: 1.  
 DR SMART; SM00406; Igv: 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 98 V SEGMENT.  
 FT DOMAIN 99 104 D SEGMENT.  
 FT DOMAIN 105 118 J SEGMENT.  
 FT DISULFID 22 96 BY SIMILARITY.  
 FT NON\_TER 118 118  
 SQ SEQUENCE 118 AA; 12934 MW; 94F7BEE4C762A018 CRC64;

Query Match 69.2%; Score 425; DB 1; Length 118;  
 Best Local Similarity 68.6%; Pred. No. 9.2e-37;  
 Matches 81; Conservative 14; Mismatches 21; Indels 2; Gaps 1;  
 QY 1 QVQLQSGAEIVRPGTSVKVCKASGYAFTNYLIEWVKORPGQGLEWIGVINPGSGGTNY 60  
 DB 1 EVQLQQSGPELVKPKASVKISCKASGYFTTDYIMWVKQSHGKLSLEWIGDINPNNGGTSY 60

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RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RL antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PTR; B02034; HWMS61.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT STGNAL 1
FT CHAIN 19 IG HEAVY CHAIN V REGION 186-1.
FT FT CHAIN 20 117 FRAMEWORK 1.
FT FT DOMAIN 20 49 FRAMEWORK 1.
FT FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT FT DOMAIN 55 68 FRAMEWORK 2.
FT FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT FT DOMAIN 86 117 FRAMEWORK 3.
FT FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
FT SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 67.4%; Score 414; DB 1; Length 117;
Best Local Similarity 79.68; Pred. No. 1.2e-35;
Matches 78; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 QVQLQQSGAEIVRPTGSVKYKSGAGVAYNYLIEWVKRPGQGGLGVINPGSGGTNY 60
DB 20 QVQLQQSGAEIVRPGASVKLSCKASGYTFYSYMHVWKQRPGRGLEWIGRIDPNSGGTKY 79
QY 61 NEKPKGKATLTADKSSSTAYMQJSSLTSDSDSAVYFCAR 98
DB 80 NEKPKSKATLTVDTSSTAYMQLSLTSDSAVYFCAR 117

RESULT 15
HV05_MOUSE STANDARD; PRT; 117 AA.
ID HV05_MOUSE
AC P01749;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 3 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPB family of
RL antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
DR PTR; B02034; HWMS61.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT STGNAL 1
FT CHAIN 19 IG HEAVY CHAIN V REGION 186-1.
FT FT CHAIN 20 117 FRAMEWORK 1.
FT FT DOMAIN 20 49 FRAMEWORK 1.
FT FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT FT DOMAIN 55 68 FRAMEWORK 2.
FT FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT FT DOMAIN 86 117 FRAMEWORK 3.
FT FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
FT SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

```



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GenCore version 4.5  
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OM protein - protein search, using sw model  
Run on: December 27, 2001, 09:00:04 ; Search time 38.99 Seconds  
(without alignments)  
435.178 Million cell updates/sec

Title: US-09-889-300A-1  
Perfect score: 614  
Sequence: 1 QVQLQSGAELVPCPSVKV.....ARDGPFAYWGQGLTVTVSA 116

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues  
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_17:\*

- 1: sp.archaea:\*
- 2: sp.bacteria:\*
- 3: sp.fungi:\*
- 4: sp.human:\*
- 5: sp.invertebrate:\*
- 6: sp.mammal:\*
- 7: sp.mhc:\*
- 8: sp.organelle:\*
- 9: sp.phage:\*
- 10: sp.plant:\*
- 11: sp.rodent:\*
- 12: sp.virus:\*
- 13: sp.vertebrate:\*
- 14: sp.unclassified:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	526.5	85.7	473	11 Q9D8L4	Q9D8L4 mus musculus
2	477	77.7	463	11 Q9D8L4	Q9D8L4 mus musculus
3	458.5	74.7	117	11 Q9QXF0	Q9QXF0 mus musculus
4	457	74.4	118	11 Q9Z1C4	Q9Z1C4 mus musculus
5	453.5	73.9	117	11 Q9QXE9	Q9QXE9 mus musculus
6	453	73.8	473	11 Q9D8L4	Q9D8L4 mus musculus
7	449	73.1	109	11 Q9JL75	Q9JL75 mus musculus
8	435.5	70.9	117	11 Q9Z1C6	Q9Z1C6 mus musculus
9	429	69.9	110	11 Q9JL83	Q9JL83 mus musculus
10	422	68.7	111	11 Q9D9B8	Q9D9B8 mus musculus
11	415.5	67.7	119	4 Q9UL94	Q9UL94 homo sapien
12	411	66.9	110	11 Q9JL77	Q9JL77 mus musculus
13	406	66.1	114	11 Q9JL81	Q9JL81 mus musculus
14	404.5	65.9	468	11 Q9JL31	Q9JL31 mus musculus
15	404	65.8	124	4 Q9UL92	Q9UL92 homo sapien
16	403.5	65.7	125	4 Q9UL95	Q9UL95 homo sapien
17	402.5	65.6	119	5 Q9GZ22	Q9GZ22 schistosoma
18	373	60.7	116	4 Q9UL89	Q9UL89 homo sapien
19	367.5	59.9	157	4 Q95978	Q95978 homo sapien

RESULT	1	500	4	Q9BRV0	Q9BRV0 homo sapien
20	362	59.0	109	11 Q9JL85	Q9JL85 mus musculus
21	359.5	58.6	150	4 Q9Y298	Q9Y298 homo sapien
22	355.5	57.9	484	11 Q99LA6	Q99LA6 mus musculus
23	328.5	53.5	298	11 Q9QYF0	Q9QYF0 mus musculus
24	328	53.4	102	11 Q9JL79	Q9JL79 mus musculus
25	312.5	50.9	120	4 Q9BUA1	Q9BUA1 homo sapien
26	310	50.5	113	4 Q9UL90	Q9UL90 homo sapien
27	309.5	50.4	112	4 Q9HCC1	Q9HCC1 homo sapien
28	309	50.3	147	4 Q9Y509	Q9Y509 homo sapien
29	309	50.3	116	4 Q9UL93	Q9UL93 homo sapien
30	308.5	50.2	487	11 Q99KA4	Q99KA4 mus musculus
31	307	50.0	119	4 Q9UL73	Q9UL73 homo sapien
32	302.5	49.3	122	4 Q9UL84	Q9UL84 homo sapien
33	302	49.2	124	6 Q9N0W6	Q9N0W6 oryctolagus
34	301	49.0	124	6 Q9N0W4	Q9N0W4 oryctolagus
35	299	48.7	437	11 Q9RIA4	Q9RIA4 mus musculus
36	298	48.5	121	4 Q9UL71	Q9UL71 homo sapien
37	295.5	48.1	131	4 Q9UL88	Q9UL88 homo sapien
38	290.5	47.3	118	4 Q9UL91	Q9UL91 homo sapien
39	290	47.2	118	4 Q9UL72	Q9UL72 homo sapien
40	290	47.2	479	11 Q99M22	Q99M22 mus musculus
41	289.5	47.1	597	4 Q9BU10	Q9BU10 homo sapien
42	278.5	45.4	121	11 Q99NG4	Q99NG4 mus musculus
43	277	45.1	597	4 Q9BOB8	Q9BOB8 homo sapien
44	274.5	44.7	112	4 Q9UGP3	Q9UGP3 homo sapien
45	273.5	44.5			

## ALIGNMENTS

Q9D8L4 PRELIMINARY: PRT: 473 AA.

AC Q9D8L4; 01-JUN-2001 (TREMREL. 17, Created)

DT 01-JUN-2001 (TREMREL. 17, Last sequence update)

DT 01-JUN-2001 (TREMREL. 17, Last annotation update)

DE 1810060009RIK PROTEIN.

GN 1810060009RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=PANCREAS;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-Oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kotsuki S.,

RA Hayashizaki Y.;

RA "Functional annotation of a full-length mouse cdna collection.";

Nature 409:685-690(2001).

CC -i- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX

CC DOMAIN.

EMBL; AK007918; BAB25349.1; -

DR MGD; MGI:1924014; 1810060009RIK.

DR InterPro; IPR003599; Ig.

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DR InterPro: IPR003597; Ig-cl.
DR InterPro: IPR003600; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 4.
DR SMART: SM00409; Ig; 2.
DR SMART: SM00407; Igcl; 3.
DR SMART: SM00406; IgV; 1.
DR SMART: SM00410; Ig-like; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FB8 CRC64;

Query Match 85.7%; Score 526.5; DB 11; Length 473;
Best Local Similarity 84.9%; Pred. No. 2.1e-46;
Matches 101; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 20 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLIEWVKORPGGLEWIGVINPGSGGTNY 79
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAYVFCARDG---PWFAYWGQGLTVTVA 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAYVFCARSDYDWFAYWGQGLTVTVA 138
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
Q99LC4 PRELIMINARY; PRT; 463 AA.
ID Q99LC4;
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1;
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6B8C30783 CRC64;

Query Match 77.7%; Score 477; DB 11; Length 463;
Best Local Similarity 77.5%; Pred. No. 2.7e-41;
Matches 93; Conservative 7; Mismatches 16; Indels 4; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 20 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLIEWVKORPGGLEWIGVINPGSGGTNY 79
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAYVFCARDGPW---FAYWGQGLTVTVA 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 80 SEKFKGKATLTADKSSSTAYMQLSSLTSDSAYVFCARSSYSDYDLFAYWGQGLTVTVA 139
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
Q9QXF0 PRELIMINARY; PRT; 117 AA.
ID Q9QXF0;
AC Q9QXF0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
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RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
   DOMAIN
DR EMBL; AJ225171; CAB65236.1;
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13060 MW; D816AD0858A47E4C CRC64;

Query Match 74.7%; Score 458.5; DB 11; Length 117;
Best Local Similarity 73.5%; Pred. No. 4.4e-40;
Matches 86; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 EVQLQSGPELVKPGASVKMSCKASGYTFDYIMKVKVKGSHGKSLIEWIGDINPNGGTSY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAYVFCARDGP-WFAYWGQGLTVTVA 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 NQKFKGKATLTVDKSSSTAYMQLSSLTSDSAYVFCARDKYDFYWGQGLTLTVSS 117
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
Q9Z1C4 PRELIMINARY; PRT; 118 AA.
ID Q9Z1C4;
AC Q9Z1C4;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
DE ANTI-PORCINE VCAM MAB 3F4 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Mattis L.M., Evans M.J.;
RT "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
RT IgG2/G4 constant regions block human leukocyte binding to porcine
RT endothelial cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
   DOMAIN
DR EMBL; U78801; AAD00293.1;
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
DR NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 13036 MW; 90EEC559D31EC4FC CRC64;

Query Match 74.4%; Score 457; DB 11; Length 118;
Best Local Similarity 73.7%; Pred. No. 6.4e-40;
Matches 87; Conservative 13; Mismatches 16; Indels 2; Gaps 1;

QY 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 QVQLQSGAELVRPGTSVKVSKASGYAFTNLYLIEWVKORPGGLEWIGVINPGSGGTNY 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAYVFCARD--GWFAFYWGQGLTVTVA 116
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TQKFRGKATLTADKSSSTAYMQLSSLTSDSAYVFCARVTGCGYDFYWGQGLTLTVSS 118
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 5
OQ0XE9 PRELIMINARY: PRT: 117 AA.
ID OQ0XE9
AC OQ0XE9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN V-D-J REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Clemens A., Rademaekers A., Specht C., Koelsch E.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AJ225117; CAB65237.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
FT NON_TER 1
FT NON_TER 117
SQ SEQUENCE 117 AA; 13000 MW; CDDE2AF84D499734 CRC64;

Query Match 73.9%; Score 453.5; DB 11; Length 117;
Best Local Similarity 73.7%; Pred. No. 1.5e-39;
Matches 87; Conservative 16; Mismatches 12; Indels 3; Gaps 2;

Oy 1 QVQLQQSGAEIVRPGTSVKVSKASGYAFTNYLIWVKQKPGQGLEWIGVINPGSGGTNY 60
Db 1 EVQLQQSGPELVKPGASVKMSCKASGYFTDYMKNVKQSKGLEWIGDINPNNGGTSY 60

Oy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGPWFA--YWGQGTFLVTVSA 116
Db 1 NEKFKGKATLTVDKSSSTAYMQLNSLTSDSAVYCARD-RYAYMDYWGQGTSTVTVSS 117

RESULT 6
OQ9L25 PRELIMINARY: PRT: 473 AA.
ID OQ9L25
AC OQ9L25;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC003888; AAH03888.1; -.
SQ SEQUENCE 473 AA; 52449 MW; BE9889B7986DA155 CRC64;

Query Match 73.8%; Score 453; DB 11; Length 473;
Best Local Similarity 71.0%; Pred. No. 8.5e-39;
Matches 88; Conservative 10; Mismatches 18; Indels 8; Gaps 1;

Oy 1 QVQLQQSGAEIVRPGTSVKVSKASGYAFTNYLIWVKQKPGQGLEWIGVINPGSGGTNY 60
Db 20 QVQLQQSDAEIVKPGASVKISKVSGYFTDTHWVKQKPGQGLEWIGYIYPRDGSFKY 79

Oy 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCARDGP-----WPAFYWGQGTFLV 112
Db 80 NEKFKGKATLTADKSSSTAYMQLNSLTSDSAVCFCSRGGSIYGYGLYFDYWGQGTTI 139
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Qy 113 TVSA 116
Db 140 TVSS 143

RESULT 7
OQJL75 PRELIMINARY: PRT: 109 AA.
ID OQJL75
AC OQJL75;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RL "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis."
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF206031; AAF69329.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IgV; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 12118 MW; FF65E441BBF936A6 CRC64;

Query Match 73.1%; Score 449; DB 11; Length 109;
Best Local Similarity 76.1%; Pred. No. 3.9e-39;
Matches 83; Conservative 14; Mismatches 10; Indels 2; Gaps 1;

Oy 10 ELVRPGTSVKVSKASGYAFTNYLIWVKQKPGQGLEWIGVINPGSGGTNYNEKPKGRAT 69
Db 1 ELVKPGASVKMSCKASGYFTSYVHHVVKQKPGQGLEWIGYINPYNDGTNYNEKPKGRAT 60

Oy 70 LTADKSSSTAYMQLSSLTSDSAVYFCARDGPW--FAYWGQGTFLVTVSA 116
Db 61 LTSDKSSSTAYMQLSSLTSDSAVYCARDGNRYRFGDYWGQGTTLTVSS 109

RESULT 8
OQZIC6 PRELIMINARY: PRT: 117 AA.
ID OQZIC6
AC OQZIC6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ANTI-PORCINE VCAM MAB 2A2 HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Mueller J.P., Giannoni M.A., Hartman S.L., Elliott E.A., Squinto S.P.,
RA Matis L.M., Evans M.J.;
RL "Humanized porcine VCAM-specific monoclonal antibodies with chimeric
IG2/G4 constant regions block human leukocyte binding to porcine
endothelial cells."
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: U78799; AAD00291.1; -.

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DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig: 1.  
DR SMART: SM00406; IGV: 1.  
FT NON\_TER 1  
FT 117  
SQ SEQUENCE 117 AA; 13122 MW; 4F65B193AFB77E5B CRC64;

Query Match 70.9%; Score 435.5; DB 11; Length 117;  
Best Local Similarity 70.1%; Pred. No. 1.1e-37;  
Matches 82; Conservative 13; Mismatches 21; Indels 1; Gaps 1;  
QY 1 QVLOQSGAELVPRGTSVKVSKKASGYAFNTNLYIEWVKORPGOGLEWIGVINPFGSGGTNY 60  
DB 1 QVLOQSGPQLVRPGTSVKISKASGYTSFSTVMMHWVKORPGODLEWIGMIDPDSSEVKL 60  
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCAR-DGFWFAYWGQGLTVTVA 116  
DB 61 NQRLKDKAILTVDKSSNTAYMQFGTSSEDSAVYCTRGVSNFAYWGQGLTVTVA 117

RESULT 9  
Q9JL83 PRELIMINARY; PRT; 110 AA.  
AC Q9JL83;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/C;  
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-acetyl-glucosamine antibodies from mice with autoimmune myocarditis."  
RT acetyl-glucosamine antibodies from mice with autoimmune myocarditis.  
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.  
EMBL: AF206023; AAF69321.1; -.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig: 1.  
DR SMART: SM00406; IGV: 1.  
FT NON\_TER 1  
FT 110  
SQ SEQUENCE 110 AA; 12052 MW; 84E6F2AD219AF95E CRC64;

Query Match 69.9%; Score 429; DB 11; Length 110;  
Best Local Similarity 78.2%; Pred. No. 4.7e-37;  
Matches 86; Conservative 4; Mismatches 16; Indels 4; Gaps 2;

QY 10 ELVPRGTSVKVSKKASGYAFNTNLYIEWVKORPGOGLEWIGVINPFGSGGTNYNEKFKGAT 69  
DB 2 ELVKPGASVKISKASGYTSFSTVMMHWVKORPGOGLEWIGRIYIPGDGDAYNGKFKGAT 61  
QY 70 LTADKSSSTAYMQLSSLTSDSAVYFCARDPW---FAYWGQGLTVTVA 116  
DB 62 LTADKSSSTAYMQLSSLTSDSAVYFCARSN-HDVRFAYWGQGLTVTVA 110

RESULT 10  
Q9D9B8 PRELIMINARY; PRT; 111 AA.  
AC Q9D9B8;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE ADULT MALE TESTIS CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,  
DE CLONE:1700110L11, FULL INSERT SEQUENCE.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=TESTIS;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
RA Saito K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.,  
RA Nature 409:685-690(2001).  
RL "Functional annotation of a full-length mouse cDNA collection."  
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.  
EMBL: AK007163; BAB24877.1; -.  
DR InterPro: IPR003599; Ig.  
DR InterPro: IPR003600; Ig\_Like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig: 1.  
DR SMART: SM00409; IGV: 1.  
DR SMART: SM00406; IGV: 1.  
DR SMART: SM00410; IG\_Like: 1.  
SQ SEQUENCE 111 AA; 11976 MW; 874DDDF7BD98BD7B2 CRC64;

Query Match 68.7%; Score 422; DB 11; Length 111;  
Best Local Similarity 82.7%; Pred. No. 2.5e-36;  
Matches 81; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 QVLOQSGAELVPRGTSVKVSKKASGYAFNTNLYIEWVKORPGOGLEWIGVINPFGSGGTNY 60  
DB 7 QVLOQSGPQLVRPGTSVKISKASGYTSFSTVMMHWVKORPGOGLEWIGRIYIPGDGDTNY 66  
QY 61 NEKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCAR 98  
DB 67 NGKFKGKATLTADKSSSTAYMQLSSLTSDSAVYFCAR 104

RESULT 11  
Q9UL94 PRELIMINARY; PRT; 119 AA.  
AC Q9UL94;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,



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RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF035020; AAD56256.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 119
SQ SEQUENCE 119 AA; 13205 MW; 13E64F5345F4A16E CRC64;

Query Match 67.7%; Score 415.5; DB 4; Length 119;
Best Local Similarity 66.4%; Pred. No. 1.3e-35;
Matches 79; Conservative 14; Mismatches 23; Indels 3; Gaps 1;

Qy 1 QVQLQSGAELVRPCTSVKVKSCASGYAFTNYLIEWVKQKPGQGLEWIGVINPGSGGTNY 60
Db 1 EVQLVESGAELVKPGASVKVKSCASGYFTTGYMHVVRQAFQCGLEWGWNPNSWTTNY 60

Qy 61 NEKFKGKATLTADKSSSTAYMQLSLSLTDSDSAVYFCARDGP---WFAYWGQGLTLTVSA 116
Db 61 AOKFGKVTMTKDTISISTAYWELSLRSDDTAVYYCARGGGRLWFDPWGQGLTLTVSS 119

RESULT 12
Q9JL77 PRELIMINARY; PRT; 110 AA.
AC Q9JL77;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DBA/2;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF206029; AAF69327.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 110
SQ SEQUENCE 110 AA; 12138 MW; 2EDE81FB5862C9AF CRC64;
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Query Match 66.9%; Score 411; DB 11; Length 110;
Best Local Similarity 74.1%; Pred. No. 3.4e-35;
Matches 80; Conservative 9; Mismatches 17; Indels 2; Gaps 1;
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Qy 11 LVRPCTSVKVKSCASGYAFTNYLIEWVKQKPGQGLEWIGVINPGSGGTNYNEKFKGKATL 70
Db 3 LVRPCASVKLSCKASGYFTTSWVHWAKQKPGQGLEWIGELHPNSGHTNYNEKFKGKATL 62

Qy 71 TADKSSSTAYMQLSLSLTDSDSAVYFCARDGPWFA--YWGQGLTLTVSA 116
Db 63 TVDRSSSTAYVDLSLTSLESDSAVYCARQRNRYANDYWGQGLTVTVSS 110
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RESULT 13
Q9JL81 PRELIMINARY; PRT; 114 AA.
AC Q9JL81;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "Characterization of cross-reactive monoclonal anti-myosin/anti-n-
acetyl-glucosamine antibodies from mice with autoimmune myocarditis.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF206025; AAF69323.1; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; Ig; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12829 MW; 404885FDE6BA56F8 CRC64;
```

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Query Match 66.1%; Score 406; DB 11; Length 114;
Best Local Similarity 68.1%; Pred. No. 1.2e-34;
Matches 77; Conservative 13; Mismatches 17; Indels 6; Gaps 1;

Qy 10 ELVRPCTSVKVKSCASGYAFTNYLIEWVKQKPGQGLEWIGVINPGSGGTNYNEKFKGKAT 69
Db 2 QLVRPGASVKISCRASGYFTSYNHHVVKQKPGQGLEWIGMDPSDSETRLNQKPKDKAT 61

Qy 70 LTAKSSSTAYMQLSLSLTDSDSAVYFCARDG-----PWFAWGQGLTLTVSA 116
Db 62 LTVDKSSSTAYMQLSSPTSEDSAVYCARSNYGSLSYFYDWGQGLTLTVSS 114
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RESULT 14
Q99L31 PRELIMINARY; PRT; 468 AA.
AC Q99L31;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC003878; AAH03878.1; -.
SQ SEQUENCE 468 AA; 51661 MW; 96352328B332ADB CRC64;
```

```
Query Match 65.9%; Score 404.5; DB 11; Length 468;
Best Local Similarity 64.7%; Pred. No. 8.7e-34;
Matches 77; Conservative 19; Mismatches 20; Indels 3; Gaps 1;

Qy 1 QVQLQSGAELVRPCTSVKVKSCASGYAFTNYLIEWVKQKPGQGLEWIGVINPGSGGTNY 60
Db 20 EVQLQSGAELVRPGASVKLSCKASGYFTSGFNKDSLHWVQKQKPGQGLEWIGWIDPEDGETKY 79

Qy 61 NEKFKGKATLTADKSSSTAYMQLSLSLTDSDSAVYFCARD---GPWFAYWGQGLTLTVSA 116
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GenCore version 4.5  
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OM protein - protein search, using sw model  
Run on: December 27, 2001, 09:03:33 ; Search time 14.63 seconds  
(without alignments)  
268.157 Million cell updates/sec

Title: US-09-889-300A-2  
Perfect score: 562  
Sequence: 1 NIVMTQSPKSMMSVCGERT.....CGQGYSPYTFGGTKLEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues  
Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					%		Description	
Result No.	Score	Match	Length	ID				
1	562	100.0	136	1	KV5B_MOUSE		P01634	mus musculus
2	422	75.1	149	1	KV5A_MOUSE		P01633	mus musculus
3	403	71.7	114	1	KV1A_MOUSE		P01632	mus musculus
4	383	68.1	114	1	KV4A_HUMAN		P01625	homo sapien
5	376	66.9	134	1	KV4C_HUMAN		P06314	homo sapien
6	375	66.7	108	1	KV1M_HUMAN		P01605	homo sapien
7	370	65.8	108	1	KV1Y_HUMAN		P80362	homo sapien
8	365	64.9	108	1	KV1O_HUMAN		P01607	homo sapien
9	363	64.6	108	1	KV1V_HUMAN		P04430	homo sapien
10	362.5	64.5	133	1	KV4B_HUMAN		P06313	homo sapien
11	359	63.9	108	1	KV1H_HUMAN		P01600	homo sapien
12	359	63.9	111	1	KV3J_MOUSE		P01662	mus musculus
13	359	63.9	129	1	KV1L_HUMAN		P04432	homo sapien
14	358	63.7	108	1	KV1L_HUMAN		P01604	homo sapien
15	358	63.7	111	1	KV3H_MOUSE		P01660	mus musculus
16	358	63.7	129	1	KV1W_HUMAN		P04431	homo sapien
17	357	63.5	108	1	KV1N_HUMAN		P01606	homo sapien
18	356.5	63.4	129	1	KV3M_HUMAN		P18136	homo sapien
19	355.5	63.3	129	1	KV3L_HUMAN		P18135	homo sapien
20	354	63.0	131	1	KV3L_MOUSE		P01661	mus musculus
21	353	62.8	108	1	KV1E_MOUSE		P01597	homo sapien
22	353	62.8	111	1	KV3L_MOUSE		P01664	mus musculus
23	352.5	62.7	109	1	KV3B_HUMAN		P01620	homo sapien
24	352.5	62.7	109	1	KV1A_HUMAN		P01624	homo sapien
25	350	62.3	108	1	KV1A_HUMAN		P01593	homo sapien
26	349.5	62.2	109	1	KV3E_HUMAN		P01623	homo sapien
27	349	62.1	108	1	KV1K_HUMAN		P01603	homo sapien
28	349	62.1	108	1	KV1P_HUMAN		P01608	homo sapien
29	348	61.9	108	1	KV1B_HUMAN		P01594	homo sapien
30	348	61.9	108	1	KV1S_HUMAN		P01611	homo sapien
31	348	61.9	108	1	KV5M_MOUSE		P01646	mus musculus
32	347	61.7	108	1	KV1R_HUMAN		P01610	homo sapien
33	344.5	61.3	129	1	KV3H_HUMAN		P04207	homo sapien

34	343.5	61.1	109	1	KV3D_HUMAN		P01622	homo sapien
35	343	61.0	111	1	KV3K_MOUSE		P01663	mus musculus
36	342.5	60.9	113	1	KV2G_MOUSE		P01631	mus musculus
37	342	60.9	108	1	KV1G_HUMAN		P01599	homo sapien
38	342	60.9	108	1	KV1Q_HUMAN		P01609	homo sapien
39	342	60.9	108	1	KV5U_MOUSE		P04946	mus musculus
40	342	60.9	111	1	KV3M_MOUSE		P01665	mus musculus
41	341	60.7	108	1	KV1C_HUMAN		P01595	homo sapien
42	341	60.7	108	1	KV5K_MOUSE		P01644	mus musculus
43	339.5	60.4	108	1	KV3A_HUMAN		P01619	homo sapien
44	339	60.3	111	1	KV3D_MOUSE		P03977	mus musculus
45	339	60.3	111	1	KV3O_MOUSE		P01667	mus musculus

# ALIGNMENTS

```

RESULT      1
KV5B_MOUSE
ID   KV5B_MOUSE          STANDARD;          PRT;   136 AA.
AC   P01634;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DE   IG KAPPA CHAIN V-V REGION MOPC 21 PRECURSOR.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=82059477; PubMed=6170937;
RA   Hamlyn P.H., Gait M.J., Milstein C.;
RT   "Complete sequence of an immunoglobulin mRNA using specific priming
RT   and the dideoxynucleotide method of RNA sequencing.";
RL   Nucleic Acids Res. 9:4485-4494(1981).
RN   [2]
RP   SEQUENCE OF 30-136.
RX   MEDLINE=73054310; PubMed=4638343;
RA   Svastli J., Milstein C.;
RT   "The complete amino acid sequence of a mouse kappa light chain.";
RL   Biochem. J. 128:427-444(1972).
-----
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DR   EMBL: V00810; CAA24192.1; ALT_TERM.
DR   PIR: A01917; KVM521.
DR   InterPro: IPR003006; Ig_MHC.
DR   InterPro: IPR003596; Ig_V.
DR   Pfam: PF00047; Ig; 1.
DR   SMART: SM00406; IgV; 1.
KW   Immunoglobulin V region; Signal.
FT   SIGNAL      1..29
FT   CHAIN       30..136  IG KAPPA CHAIN V-V REGION MOPC 21.
FT   DOMAIN      30..52  FRAMEWORK 1.
FT   DOMAIN      53..63  COMPLEMENTARITY-DETERMINING 1.
FT   DOMAIN      64..78  FRAMEWORK 2.
FT   DOMAIN      79..85  COMPLEMENTARITY-DETERMINING 2.
FT   DOMAIN      86..117 FRAMEWORK 3.
FT   DOMAIN      118..126 COMPLEMENTARITY-DETERMINING 3.
FT   DOMAIN      127..136 FRAMEWORK 4.
FT   NON_TER     136
SQ   SEQUENCE 136 AA; 14902 MW; 8CDD85113996D1C2 CRC64;

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Query Match 100.0%; Score 562; DB 1; Length 136;  
Best Local Similarity 100.0%; Pred. No. 8.9e-54;

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FT REPEAT      26      35
FT REPEAT      38      47
FT NON_TER     149
SQ SEQUENCE    149 AA; 16434 MW;  B0480C87B682AC3E CRC64;

Query Match      75.1%; Score 422; DB 1; Length 149;
Best Local Similarity 78.5%; Pred. No. 1.3e-38;
Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 NIYMTQSPKSMMSVGRVTLTKASENVVTVYSWYQOKPEQSPKLLIYGASNRYTGVDP 60
   :||||| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 42 DIVMTQSHKFMSTVSGDRSVITCKASQDVTVAWYQOKPEQSPKLLIYSASYRTGVDP 101

QY 61 RFTGSSATDFTTISSVQAEADLADYHCGOGYSYPYTFGGGKTLEIK 107
   :||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 102 RFTGSGGDTFTTISSVQAEADLAVVYCOQHYSYTPPTFGGKTLEIK 148

RESULT 3
KVIA_MOUSE STANDARD; PRT; 114 AA.
ID KVIA_MOUSE
AC P01632;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 08, Last annotation update)
DE IG KAPPA CHAIN V-I REGION S107A.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81241357; PubMed=6798890;
RA Kwan S.-P., Rudikoff S., Seidman J.G., Leder P., Scharff M.D.;
RT "Nucleic acid and protein sequences of phosphocholine-binding light
   chains."
RL J. Exp. Med. 153:1366-1370(1981).
-----
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CC EMBL; U29423; AAC00033.1; -.
CC PIR; A01915; KVM57A.
CC HSP; P01789; 2MCP.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig_1.
CC SMART; SM00406; IGV; 1..
CC Immunoglobulin V region.
KW DOMAIN 1 23
FT DOMAIN 1 23
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 41 55 FRAMEWORK 2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 63 94 FRAMEWORK 3.
FT DOMAIN 95 103 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 104 113 FRAMEWORK 4.
FT DISULFID 123 94 BY SIMILARITY.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12717 MW; 32008EC8E9DBE67B CRC64;

Query Match      71.7%; Score 403; DB 1; Length 114;
Best Local Similarity 67.3%; Pred. No. 1e-36;
Matches 76; Conservative 16; Mismatches 15; Indels 6; Gaps 1;

QY 1 NIYMTQSPKSMMSVGRVTLTKASENV-----VTVYSWYQOKPEQSPKLLIYGASNR 54
   :||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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RA Capra J.D., Klapper D.G.;  
RT "Complete amino acid sequence of the variable domains of two human  
RT IgM anti-gamma globulins (Lay/Pom) with shared idiotype  
RT specificities";  
RL Scand. J. Immunol. 5:677-684(1976).  
CC -I- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS  
CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,  
CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.  
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA  
CC GLOBULIN ACTIVITY.  
DR PIR; A01871; KIHULE.  
DR HSP; P01607; IREI.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULFID 23 88  
FT CONFLICT 30 31  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;

Query Match 66.7%; Score 375; DB 1; Length 108;  
Best Local Similarity 65.4%; Pred. No. 1e-33;  
Matches 70; Conservative 18; Mismatches 19; Indels 0; Gaps 0;

QY 1 NIWVTQSPKSMVSGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTVGPD 60  
DB 1 DIQMTQSPSLVSGVDRVITTCQASQNVNAYLNWYQKPGAPKLLIYGASTREAGVPS 60  
QY 61 RFTGSGSATDFTLTSSVQAEADLYHCGQGYSPYPTFGGKLEIK 107  
DB 61 RFTGSGSGTDTFTTSSLPEDIATYCCQYNNWPTFGGKTVK 107

RESULT 7  
KVLY\_HUMAN STANDARD; PRT; 108 AA.  
AC P80362;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-I REGION WAT.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).  
RX MEDLINE=95086080; PubMed=7993911;  
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,  
RA Solomon A., Stevens F.J., Schiffer M.;  
RT "Comparison of crystal structures of two homologous proteins:  
RT structural origin of altered domain interactions in immunoglobulin  
RT light-chain dimers";  
RL Biochemistry 33:14848-14857(1994).  
RN [2]  
RP SEQUENCE OF 1-35.  
RX MEDLINE=81267384; PubMed=6167731;  
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,  
RA Popp R.A., Solomon A.;  
RT "Characterization and preliminary crystallographic data on the VL-  
RT related fragment of the human kappa Bence Jones protein Wat.";  
RL J. Mol. Biol. 147:185-193(1981).  
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PDB; 1WTL; 01-NOV-94.

DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULFID 23 88  
FT CONFLICT 30 31  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FA5697 CRC64;  
Query Match 65.8%; Score 370; DB 1; Length 108;  
Best Local Similarity 63.6%; Pred. No. 3.5e-33;  
Matches 68; Conservative 20; Mismatches 19; Indels 0; Gaps 0;  
QY 1 NIWVTQSPKSMVSGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTVGPD 60  
DB 1 DIQMTQSPSLVSGVDRVITTCRASQDITVYVWYQKPGAPKLLIYGASILETGVP 60  
QY 61 RFTGSGSATDFTLTSSVQAEADLYHCGQGYSPYPTFGGKLEIK 107  
DB 61 RFTGSGSGTDTFTTSSLPEDIATYCCQYDTLTLTFGGKTVK 107  
RESULT 8  
KVIO\_HUMAN STANDARD; PRT; 108 AA.  
AC P01607;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-I REGION REI.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=76023758; PubMed=809329;  
RA Palm W., Hilschmann N.;  
RT "The primary structure of a crystalline monoclonal immunoglobulin  
RT kappa-type L-chain, subgroup 1 (Bence-Jones protein Re1.); isolation  
RT and characterization of the tryptic peptides; the complete amino acid  
RT sequence of the protein; a contribution to the elucidation of the  
RT three-dimensional structure of antibodies, in particular their  
RT combining site.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).  
RN [2]  
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).  
RX MEDLINE=76039968; PubMed=1182131;  
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;  
RT "The molecular structure of a dimer composed of the variable portions  
RT of the Bence-Jones protein REI refined at 2.0-A resolution.";  
RL Biochemistry 14:4943-4952(1975).  
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1.2)  
CC MARKER.  
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR; A01873; KIHURE.  
DR PDB; IREI; 17-FEB-84.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_V.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULFID 23 88  
FT CONFLICT 30 31  
FT NON\_TER 108 108  
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FA5697 CRC64;

```
FT DOMAIN 35 49 FRAMEWORK 2
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 FRAMEWORK 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT TURN 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 64.9%; Score 365; DB 1; Length 108;
Best Local Similarity 63.2%; Pred. No. 1.2e-32;
Matches 67; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMNSGVRVTLTKASENVVTVSVYQOKPEQSKLLIYGASNRVTGVPD 60
: ||||| |::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1 DIQMTQSPSSLASVSDRVITTCASQSDIIKYLNNYQQTTPGKAPKLLIYEASNLQAGVPS 60
||:|||| |::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 61 RTQSGSATDFTLTSSVQAEADLADYHCGQGYSPYPTGGGKLEIK 107
||||| ||| |||||::|||::|||::|||::|||::|||::|||::|||::|||
Db 61 NFTSGSGTDFLTITSSLPQEDFATYYCQYNSYPYTFGGTKVQIK 107
||||| ||| |||||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 10
KV4B_HUMAN
ID KV4B_HUMAN STANDARD; PRT; 133 AA.
AC P06313;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-IV REGION JI PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combratio G., Mocikat R., Pohlenz H.D.,
RA Zschau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
single germline gene."
RL Nucleic Acids Res. 13:6515-6529(1985).
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CC -----
CC EMBL; Z00022; CAA77317.1; -.
DR PIR; A01904; K4HUJ1.
DR HSSP; P01789; 2MCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 61 75 FRAMEWORK 2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 83 114 FRAMEWORK 3.
FT DOMAIN 115 122 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 123 132 FRAMEWORK 4.
FT DISULFID 43 114 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 64.5%; Score 362.5; DB 1; Length 133;
Best Local Similarity 63.7%; Pred. No. 2.9e-32;
Matches 72; Conservative 19; Mismatches 15; Indels 7; Gaps 2;

FT DOMAIN 35 49 FRAMEWORK 2
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 FRAMEWORK 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT TURN 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 85 90
FT STRAND 98 98
FT STRAND 102 106
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 64.9%; Score 365; DB 1; Length 108;
Best Local Similarity 63.2%; Pred. No. 1.2e-32;
Matches 67; Conservative 19; Mismatches 20; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMNSGVRVTLTKASENVVTVSVYQOKPEQSKLLIYGASNRVTGVPD 60
: ||||| |::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1 DIQMTQSPSSLASVSDRVITTCASQSDIIKYLNNYQQTTPGKAPKLLIYEASNLQAGVPS 60
||:|||| |::|||::|||::|||::|||::|||::|||::|||::|||::|||
QY 61 RTQSGSATDFTLTSSVQAEADLADYHCGQGYSPYPTGGGKLEIK 107
||||| ||| |||||::|||::|||::|||::|||::|||::|||::|||::|||
Db 61 NFTSGSGTDFLTITSSLPQEDFATYYCQYNSYPYTFGGTKVQIK 107
||||| ||| |||||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 9
KV1V_HUMAN
ID KV1V_HUMAN STANDARD; PRT; 108 AA.
AC P04430;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION BAN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=86174817; PubMed=3083240;
RA Dwulet F.E., O'Connor T.P., Benson M.D.;
RT "Polymorphism in a kappa I primary (AL) amyloid protein (BAN).";
RL Mol. Immunol. 23:73-78(1986).
DR PIR; A01878; K1HUBN.
DR HSSP; P80362; 1WPL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Amyloid.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
```

QY 1 NIWVTSQPKSMSSVGERVTLTKASENVV-----TVSWYQKPEQSPKLLIYGASNR 54  
 DB 21 DIVMTQSPDSLAVSLGERATINCKSSQVLYSSNNKNYLAQYQKPGQPPKLLIYWASPR 80  
 QY 55 YGVDPDRFTGSGSATDFTLTISVQAEDLADYHCGGYGYPTFTGGGKLEIK 107  
 DB 81 ESGVDPDRFSGSGSDFTLTISLQAEADVAVYCOQYDIP-TFGGKTRVEIK 132

RESULT 11  
 KVIH\_HUMAN STANDARD; PRT; 108 AA.  
 AC P01600;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-I REGION HAU.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=71032830; PubMed=4097974;  
 RA Watanabe S., Hilschmann N.;  
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-  
 chain of subgroup I (Bence-Jones Protein Hau): subdivision within  
 subgroups.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).  
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
 CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
 DR PIR: A01868; K1HUHU.  
 DR HSP: P80362; LWTL.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; Igv; 1.  
 KW Immunoglobulin V region; Bence-Jones protein.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34  
 FT DOMAIN 35 49  
 FT DOMAIN 50 56  
 FT DOMAIN 57 88  
 FT DOMAIN 89 97  
 FT DOMAIN 98 107  
 FT DOMAIN 107 108  
 FT DISULFID 23 88  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A616D8D0618 CRC64;

Query Match 63.9%; Score 359; DB 1; Length 108;  
 Best Local Similarity 61.7%; Pred. No. 5.4e-32;  
 Matches 66; Conservative 22; Mismatches 19; Indels 0; Gaps 0;

QY 1 NIWVTSQPKSMSSVGERVTLTKASENVVTVSWYQKPEQSPKLLIYGASNRVTVGVPD 60  
 DB 1 DIQWTSPLSASVGDRTVITCRASQSSISLSWYQKPKAPQVLIYAASLPSGVPS 60  
 QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGGYGYPTFTGGGKLEIK 107  
 DB 61 RFGSGSGSDFTLTISLQAEADVAVYCOQYDIP-TFTSGGKTRVEIK 107

RESULT 12  
 KV3J\_MOUSE STANDARD; PRT; 111 AA.  
 AC P01662;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-III REGION ABPC 22/PC 9245.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE (ABPC 22).  
 RX MEDLINE=79012520; PubMed=95744;  
 RA McKean D.J., Bell M., Potter M.;  
 RT "Mechanisms of antibody diversity: multiple genes encode structurally  
 related mouse kappa variable regions.";  
 RL proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
 RN [2]  
 RP SEQUENCE (PC 9245).  
 RX MEDLINE=79073152; PubMed=103003;  
 RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
 RT "Rearrangement of genetic information may produce immunoglobulin  
 diversity.";  
 RL Nature 276:785-790(1978).  
 CC -1- MISCELLANEOUS: THE ABPC22 AND PC9241 SEQUENCES ARE IDENTICAL.  
 DR PIR: A01935; KVMSM6.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR003596; Ig\_V.  
 DR Pfam: PF00047; Ig\_1.  
 DR SMART: SM00406; Igv; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 38  
 FT DOMAIN 39 53  
 FT DOMAIN 54 60  
 FT DOMAIN 61 92  
 FT DOMAIN 93 101  
 FT DOMAIN 102 111  
 FT DISULFID 23 92  
 FT NON\_TER 111 111  
 SQ SEQUENCE 111 AA; 12041 MW; D7DF0609303453CE CRC64;

Query Match 63.9%; Score 359; DB 1; Length 111;  
 Best Local Similarity 63.1%; Pred. No. 5.5e-32;  
 Matches 70; Conservative 17; Mismatches 20; Indels 4; Gaps 1;

QY 1 NIWVTSQPKSMSSVGERVTLTKASENVTVTVSWYQKPEQSPKLLIYGASNRVTV 56  
 DB 1 NIVLTQSPASLAVSLGQRTISCRASEVDSVSGSMHWYQKPGQPPKLLIYASNL 60  
 QY 57 GVPDRFTGSGSATDFTLTISVQAEDLADYHCGGYGYPTFTGGGKLEIK 107  
 DB 61 GVPARESGSGSDFTLTIDPVEADDAATYCOQNNEDPYTGGGKLEIK 111

RESULT 13  
 KVIH\_HUMAN STANDARD; PRT; 129 AA.  
 AC P04432;  
 DT 13-AUG-1987 (Rel. 05, Created)  
 DT 13-AUG-1987 (Rel. 05, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE IG KAPPA CHAIN V-I REGION DAUDI PRECURSOR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85014148; PubMed=6091049;  
 RA Klobeck H.G., Combrato G., Zachau H.G.;  
 RT "Immunoglobulin genes of the kappa light chain type from two human  
 lymphoid cell lines are closely related.";  
 RL Nucleic Acids Res. 12:6995-7006(1984).

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CC -----

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DR EMBL; X00966; CAA25478.1; ALT_TERM.  
DR PIR; A01884; K1HUDI.  
DR HSSP; P80362; 1WTL.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Igv; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION DAUDI.  
FT DOMAIN 23 45  
FT DOMAIN 23 45  
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 57 71 FRAMEWORK 2.  
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 79 110 FRAMEWORK 3.  
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.  
FT DOMAIN 120 129 FRAMEWORK 4.  
FT DISULFID 45 110 BY SIMILARITY.  
FT NON_TER 129 129  
SQ SEQUENCE 129 AA; 14235 MW; CAF076BC7E5574C8 CRC64;
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Query Match 63.9%; Score 359; DB 1; Length 129;  
Best Local Similarity 59.8%; Pred. No. 6.6e-32;  
Matches 64; Conservative 19; Mismatches 24; Indels 0; Gaps 0;  
QY 1 NIVMTQSPKSMMSGYRVTLTCKASENVVTVVSWYQQRPEQSPKLLIYGASNRVTGVPD 60  
Db 23 DIQMTQSPSSLASASGDRVTITCRAGHNITNFSWYQQRPGKAPRLIIYAVSNLQGVGPS 82  
QY 61 RTGSGSATDFTLTSSVOAEDLADYHCGQGYSPYPTFGGKLEIK 107  
Db 83 RFGSGSGAEFTLTSSLOPEDFATYVCOQYNSFSFTFGGKVDNK 129
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RESULT 14  
KVLL_HUMAN  
ID KVLL_HUMAN STANDARD; PRT; 108 AA.  
AC P01604;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-I REGION KUE.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79237924; PubMed=112021;  
RA Eulitz M., Kley H.-P., Zeitler H.-J.;  
RT "The primary structure of the Bence-Jones protein Kue. The amino acid  
sequence of the variable part of a human L-chain of the kappa-type.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 360:725-734(1979).  
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.  
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.  
DR PIR; A01870; K1HUKU.  
DR HSSP; P01607; IREI.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Igv; 1.  
DR SMART; SM00406; Igv; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DOMAIN 1 23  
FT DOMAIN 24 34 FRAMEWORK 1.  
FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 50 56 FRAMEWORK 2.  
FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 89 97 FRAMEWORK 3.  
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
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FT DOMAIN 98 107 FRAMEWORK 4.  
FT DISULFID 23 88 BY SIMILARITY.  
FT NON_TER 108 108  
SQ SEQUENCE 108 AA; 12127 MW; 906679A5D90E4E98 CRC64;  
  
Query Match 63.7%; Score 358; DB 1; Length 108;  
Best Local Similarity 61.7%; Pred. No. 6.9e-32;  
Matches 66; Conservative 20; Mismatches 21; Indels 0; Gaps 0;  
QY 1 NIVMTQSPKSMMSGYRVTLTCKASENVVTVVSWYQQRPEQSPKLLIYGASNRVTGVPD 60  
Db 1 DIQMTQSPSTQPSASGDRVTITCRASQSNINLAWYQQRPEKAPKLLIYKASTLETGVPS 60  
QY 61 RTGSGSATDFTLTSSVOAEDLADYHCGQGYSPYPTFGGKLEIK 107  
Db 61 RFGSGSGTEFTLTINSLOPDDFATYVCOQYSRYPTFGGKLDIK 107
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RESULT 15  
KV3H_MOUSE  
ID KV3H_MOUSE STANDARD; PRT; 111 AA.  
AC P01660;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE IG KAPPA CHAIN V-III REGION PC 3741/TEPC 111.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Mus.  
OX NCBI_TaxID=10090;  
RN [1]  
RP SEQUENCE (PC 3741).  
RX MEDLINE=79073152; PubMed=103003;  
RA Weigert M., Gatmaitan L., Loh E., Schilling J., Hood L.E.;  
RT "Rearrangement of genetic information may produce immunoglobulin  
RT diversity";  
RL Nature 276:785-790(1978).  
RN [2]  
RP SEQUENCE (TEPC 111).  
RX MEDLINE=79012520; PubMed=99744;  
RA McKean D.J., Bell M., Potter M.;  
RT "Mechanisms of antibody diversity: multiple genes encode structurally  
RT related mouse kappa variable regions";  
RL Proc. Natl. Acad. Sci. U.S.A. 75:3913-3917(1978).  
CC -!- MISCELLANEOUS: THE PC 3741 AND TEPC 111 SEQUENCES ARE IDENTICAL.  
DR PIR; A01934; KVMS37.  
DR InterPro; IPR003006; Ig_MHC.  
DR InterPro; IPR003596; Ig_v.  
DR Pfam; PF00047; Igv; 1.  
DR SMART; SM00406; Igv; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 38 FRAMEWORK 1.  
FT DOMAIN 39 53 COMPLEMENTARITY-DETERMINING 1.  
FT DOMAIN 54 60 FRAMEWORK 2.  
FT DOMAIN 61 92 COMPLEMENTARITY-DETERMINING 2.  
FT DOMAIN 93 101 FRAMEWORK 3.  
FT DOMAIN 102 111 COMPLEMENTARITY-DETERMINING 3.  
FT DISULFID 23 92 BY SIMILARITY.  
FT NON_TER 111 111  
SQ SEQUENCE 111 AA; 12099 MW; EC46C9D259213BE4 CRC64;
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Query Match 63.7%; Score 358; DB 1; Length 111;  
Best Local Similarity 61.3%; Pred. No. 7.1e-32;  
Matches 68; Conservative 21; Mismatches 18; Indels 4; Gaps 1;  
QY 1 NIVMTQSPKSMMSGYRVTLTCKASENVVTVVSWYQQRPEQSPKLLIYGASNRVT 56  
Db 1 DIVLTQSPASLAVSLGQRATISCRASESDYSGNFMHWYQQRPGQPPKLLIYRASNLES 60  
QY 57 GVPDRFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYPTFGGKLEIK 107
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Db 61 GIPARESGSRTDETLINPYEADVDATYCCQSNEDPYTEGGTKLEIK 111

Search completed: December 27, 2001, 09:03:33  
Job time: 209 sec



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DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 65.2%; Score 366.5; DB 4; Length 109;
Best Local Similarity 65.4%; Pred. No. 2.3e-32;
Matches 70; Conservative 20; Mismatches 16; Indels 1; Gaps 1;

QY 2 IVMTQSPKSMVSGERVTLTCKASENV-VTVSVNQKPEQSPKLLIYGASNRRTGVPD 60
Db 2 IVLTQSPGTLSSLPGERATLSCRASQSSVSSYLAWYQKPGQAPRLIYGASSRATGIPD 61
[1]
QY 61 RTGSGSATDFTLTISVQAEADLADYHCGQSYSPYTFGGGKLEIK 107
Db 62 RFSGSGGDTFTLTISRLPEDECAVYCCQYGGSSPLTFGGGTRKVEIK 108
[1]

RESULT 4
QYER29 PRELIMINARY; PRT; 107 AA.
AC Q9ER29
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ANTI HUMAN TNF-ALPHA LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Su C.Z.;
RT "Cloning and sequencing of the light chain fragment of variable region
RT genes of an anti-hTNF-a monoclonal antibody.";
RL J. Cell. Mol. Immunol. 12:21-26(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RT "Construction and sequencing of the single-chain antibody gene of a
RT human TNF-alpha specific monoclonal antibody.";
RL Ti 4 Chun i Ta Hsueh Hsueh Pao 19:373-376(1998).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL: AF262753; AAG23804.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR SMART: SM00409; IGV; 1.
FT NON_TER 107
SQ SEQUENCE 107 AA; 11784 MW; 2B15EEA6604A26C3 CRC64;

Query Match 65.1%; Score 366; DB 11; Length 107;
Best Local Similarity 64.5%; Pred. No. 2.5e-32;
Matches 69; Conservative 17; Mismatches 15; Indels 6; Gaps 1;

QY 4 MTQSPKSMVSGERVTLTCKASENV-----TYVSVNQKPEQSPKLLIYGASNRRTG 57
Db 1 MTQSPSLAMSVGKVTMCKSQSVLNSNTQKNYLAWYQKPGQPELVYFASTRSG 60
[1]
QY 58 VPDRTGSGSATDFTLTISVQAEADLADYHCGQSYSPYTFGGGKLEIK 104
Db 61 VPDRTGSGSATDFTLTISVQAEADLADYHCGQSYSPYTFGGGKLEIK 107
[1]


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QY 1 NIVMTQSPKSMMSGVGERVTLTKAKSENVTYVYVSWYQKPEQSPKLLIYGASNRV 55
DB 20 DYVMTQPLSLPVSLGDAQSISCRSQSIHVHSGNTGYLQKPGQSPKLLIYKVSNR 79
QY 56 TGVPRDFTGSGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGKLEIK 107
DB 80 SGVPRDFSGSGCTDFTLKLSRVEADLGVYCYFCGSHVPTFGSGTKLEIK 131
RESULT 7
Q9UL79 PRELIMINARY: PRT; 108 AA.
AC Q9UL79;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig.1.
DR SMART; SM00406; Igv.1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 63.5%; Score 357; DB 4; Length 108;
Best Local Similarity 60.7%; Pred. No. 2.4e-31;
Matches 65; Conservative 21; Mismatches 21; Indels 0; Gaps

QY 1 NIVMTQSPKSMMSGVGERVTLTKAKSENVTYVYVSWYQKPEQSPKLLIYGASNRV 60
DB 1 DIVMTQSPSLLSASTGDRVTISCRMSQGISLAWYQKPKGAPPELLIYAASLTQSGVPS 60
QY 61 RFTGSGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGKLEIK 107
DB 61 RFGSGSGTDFTLTISLQSEDFAFYCYQGYSPFPPTFGGQTKVEIK 107
RESULT 8
Q9UL70 PRELIMINARY: PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig.1.
DR SMART; SM00406; Igv.1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 63.5%; Score 357; DB 4; Length 108;
Best Local Similarity 60.7%; Pred. No. 2.4e-31;
Matches 65; Conservative 21; Mismatches 21; Indels 0; Gaps

QY 1 NIVMTQSPKSMMSGVGERVTLTKAKSENVTYVYVSWYQKPEQSPKLLIYGASNRV 60
DB 1 DIVMTQSPSLLSASTGDRVTISCRMSQGISLAWYQKPKGAPPELLIYAASLTQSGVPS 60
QY 61 RFTGSGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGKLEIK 107
DB 61 RFGSGSGTDFTLTISLQSEDFAFYCYQGYSPFPPTFGGQTKVEIK 107
RESULT 8
Q9UL70 PRELIMINARY: PRT; 108 AA.
AC Q9UL70;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
DOMAIN.
DR EMBL; AF035035; AAD56265.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig.1.
DR SMART; SM00406; Igv.1.
DR NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11761 MW; FB1E43E7C7AFACCC CRC64;

Query Match 64.7%; Score 363.5; DB 4; Length 109;
Best Local Similarity 65.4%; Pred. No. 4.8e-32;
Matches 70; Conservative 19; Mismatches 17; Indels 1; Gaps 1;

QY 2 IVMTQSPATLSVSPGERATLSCWASQSISSNLAWYQKPGQAPRLIYGASTRATGIPAR 61
DB 2 IVMTQSPATLSVSPGERATLSCWASQSISSNLAWYQKPGQAPRLIYGASTRATGIPAR 61
QY 62 FTGSGSATDFTLTISVQAEADLYHCGQGYSPYTFGGGKLEIK 107
DB 62 FSGSGSGTEFTLTISLQSEDFAFYHCOQYNSWPLPFTFGGQTKVEIK 108
RESULT 6
Q99M37 PRELIMINARY: PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:5947).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY TUMOR;
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002035; AAH02035.1; -.
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 64.7%; Score 363.5; DB 11; Length 238;
Best Local Similarity 59.8%; Pred. No. 1.3e-31;
Matches 67; Conservative 22; Mismatches 18; Indels 5; Gaps 1;

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RT fetus.;
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035044; AAD56280.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 63.0%; Score 354; DB 4; Length 108;
Best Local Similarity 63.6%; Pred. No. 5.le-31;
Matches 68; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 NIWVTSQPKSMMSGVGRVTLTKCKASENVVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60
Db 1 DIQMTSPSSLASVGRVTITCRASQGISNLANWYQKPKVPSLIYAASLTQSGVPS 60

QY 61 RFTGSGSATDFTLTISVQAEADLYHCQGYSPYTFGGGKLEIK 107
Db 61 RFGSGSGTDFTLTISLQAEADLYHCQGYSPYTFGGGKLEIK 107

RESULT 9
Q9UL81
ID Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035033; AAD56269.1; -.
DR HSSP; P80362; IWT.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 62.5%; Score 351.5; DB 4; Length 107;
Best Local Similarity 61.7%; Pred. No. 9.5e-31;
Matches 66; Conservative 20; Mismatches 20; Indels 1; Gaps 1;

QY 1 NIWVTSQPKSMMSGVGRVTLTKCKASENVVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60
Db 1 DIQMTSPSSLASVGRVTITCRASQGISNLANWYQKPKVPSLIYAASLTQSGVPS 60

QY 61 RFTGSGSATDFTLTISVQAEADLYHCQGYSPYTFGGGKLEIK 107
Db 61 RFGSGSGTDFTLTISLQAEADLYHCQGYSPYTFGGGKLEIK 106
```

```
RESULT 10
Q9UL83
ID Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035031; AAD56267.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 61.7%; Score 347; DB 4; Length 108;
Best Local Similarity 61.3%; Pred. No. 2.9e-30;
Matches 65; Conservative 22; Mismatches 19; Indels 0; Gaps 0;

QY 2 IVWTSQPKSMMSGVGRVTLTKCKASENVVYVSWYQKPEQSPKLLIYGASNRVTGVPDR 61
Db 2 IVWTSQPKSMMSGVGRVTLTKCKASENVVYVSWYQKPEQSPKLLIYGASNRVTGVPDR 61

QY 62 FTGSGSATDFTLTISVQAEADLYHCQGYSPYTFGGGKLEIK 107
Db 62 FSGSGSGTDFTLTISLQAEADLYHCQGYSPYTFGGGKLEIK 107

RESULT 11
Q9UL86
ID Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
CC -!- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
DR EMBL; AF035028; AAD56264.1; -.
DR HSSP; P01789; IMCP.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
```



Search completed: December 27, 2001, 09:02:32  
Job time: 148 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: December 27, 2001, 09:01:00 ; Search time 41.13 Seconds  
(without alignments)  
192.702 Million cell updates/sec

Title: US-09-889-300A-2  
Perfect score: 562  
Sequence: 1 NIVMTQSPKSMNSVGERVT.....CGQGYSPYTFGGTKLEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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21: /SIDS2/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SIDS2/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	562	100.0	107	19 AAW47086	Mouse J591 monoclonal
2	562	100.0	107	21 AAY90374	J591 monoclonal an
3	562	100.0	107	21 AAB10444	Murine monoclonal
4	562	100.0	107	22 AAB36225	Monoclonal antibod
5	562	100.0	109	13 AAR27144	IE6 kappa light ch
6	562	100.0	121	19 AAW47085	Mouse J591 monoclo
7	562	100.0	121	21 AAY90370	J591 monoclonal an
8	562	100.0	121	22 AAB36222	Murine monoclonal
9	562	100.0	127	17 AAW01145	MAB 10.1 light cha
10	527	93.8	136	17 AAW01632	Ber-H2 heavy kappa
11	521	92.7	127	21 AAY71545	Mouse AF2 antibody

12	521	92.7	136	22	AAB59693	Murine AF2 antibod
13	509	90.6	108	17	AAW00828	Variable light cha
14	482	85.8	239	16	AAW64812	ScFv anti-HCG. Mu
15	454	80.8	107	18	AAW21939	Variable light sub
16	454	80.8	107	20	AAV05271	Antibody 24-31 hum
17	449	79.9	107	20	AAV05269	Antibody 24-31 hum
18	449	79.9	133	18	AAW21934	Variable light sub
19	449	79.9	133	20	AAW05264	Antibody 24-31 hum
20	447	79.5	107	18	AAW21938	Variable light sub
21	447	79.5	107	20	AAV05270	Antibody 24-31 hum
22	447	79.5	133	18	AAW21936	Variable light sub
23	447	79.5	133	20	AAV05266	Antibody 24-31 hum
24	444	79.0	107	20	AAV05268	Antibody 24-31 hum
25	444	79.0	133	18	AAW21933	Variable light sub
26	444	79.0	133	20	AAV05263	Antibody 24-31 hum
27	441	78.5	107	13	AAW25731	Humanised VL regio
28	441	78.5	107	22	AAB69696	Human Eu antibody
29	441	78.5	128	21	AAV71547	Humanised antibody
30	432	76.9	108	21	AAB11392	Murine IIF10 VL C
31	430	76.5	116	22	AAB67070	Murine G250 antibo
32	426	75.8	120	16	AAW74969	Anti-idiotypic anti
33	424.5	75.5	108	16	AAW82970	FB5 antibody light
34	423	75.3	107	20	AAW86140	Protein sequence o
35	423	75.3	108	19	AAW48863	Murine monoclonal
36	423	75.3	132	15	AAW56961	MAB A33 light chai
37	422	75.1	107	16	AAW74959	Immunoglobulin lig
38	422	75.1	131	19	AAW62187	Mouse anti-HM1.24
39	422	75.1	131	20	AAV02545	L chain V region o
40	422	75.1	237	20	AAW95440	A33/212 single-cha
41	422	75.1	237	21	AAV54836	Linked fusion prot
42	422	75.1	241	20	AAW95441	A33/218 single-cha
43	422	75.1	241	21	AAV54837	Linked fusion prot
44	422	75.1	245	20	AAW97891	A33/218 single cha
45	422	75.1	643	19	AAW73048	A33 chimeric recep

## ALIGNMENTS

RESULT 1

AAW47086  
ID AAW47086 standard; Protein; 107 AA.

XX AC AAW47086;

XX DT 26-JUN-1998 (first entry)

XX XX Mouse J591 monoclonal antibody light chain variable region

XX DE Mouse; monoclonal antibody; J591; prostate specific membrane antigen;  
XX KW cancer; vascular endothelial cell; metastatic adenocarcinoma.

XX OS Mus sp.

XX PN W09803873-A1.

XX PD 29-JAN-1998

XX PF 17-JUL-1997; 97WO-US12035.

XX PR 09-APR-1997; 97US-0838682.

XX PR 18-JUL-1996; 96US-0022125.

XX XX (CORR ) CORNELL RES FOUND INC.

XX PA Bander NH;

XX PI WPI; 1998-120937/11.

XX DR N-PSDB; AAV13952.

XX XX Destroying cancer cells with agent that binds to prostate specific  
PT membrane antigen - on vascular endothelial cells near the cancer, or  
PT on normal, hypertrophic or cancerous prostatic cells, also used for

## PT diagnosis

PS Example 12; Page 60; 94pp; English.

XX The present sequence represents the mouse J591 monoclonal antibody light chain variable region from an example of the present invention. The chain variable region from an example of the present invention. The present invention describes the elimination of cancer cells by treating cancer cells with an agent (A) which binds to the cancer cells and destroys the cancer cells. (A) both binds to the VEC and destroys the cancer cells. Also described are: (1) the detection of cancer tissue by detecting binding of labelled (A) to VEC close to, or within, a cancer tissue; (2) eliminating or detecting normal, benignly hyperplastic or cancerous prostate epithelial cells using optionally labelled (A); (3) hybridomas that produce a monoclonal antibody (MAB) that binds to PSMA. The method is used to treat renal, urothelial, colon, lung, rectal or breast cancers and metastatic adenocarcinoma of the liver. The diagnostic method is particularly used to detect recurrence of prostatic disease or to monitor the effect of treatments for prostate cancer (presence of PSMA in the serum indicates that prostate cells are being lysed). (A) binds to an epitope of PSMA expressed on live cells (contrast antibody 7E11 which only binds after cell lysis), allowing targeting of live, unfixed cells and thus providing more efficient treatment and diagnosis. Both cancer cells themselves and the VEC on which they depend are killed. All VEC close to cancer cells express PSMA, whatever the type of cancer, but normal VEC do not.

SQ Sequence 107 AA;

Query Match 100.0%; Score 562; DB 19; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.2e-39;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIWVTQSPKSMMSVGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60

DB 1 NIWMTQSPKSMMSVGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60

QY 61 RFTGSGSATDFTLTISVQAEADLYHCGGYSPYPTFGGGTKLEIK 107

DB 61 RFTGSGSATDFTLTISVQAEADLYHCGGYSPYPTFGGGTKLEIK 107

## RESULT 2

AAY90374

ID AAY90374 standard; Protein; 107 AA.

AC AAY90374;

DT 15-JAN-2001 (first entry)

DE J591 monoclonal antibody light chain protein sequence fragment.

XX J591 monoclonal antibody; extracellular domain; diagnosis; therapy;

KW prostate specific membrane antigen; prostate cancer; light chain.

XX Homo sapiens.

XX US6107090-A.

XX 22-AUG-2000.

XX 09-APR-1997; 97US-0838682.

XX 06-MAY-1996; 96US-0016976.

XX 18-JUL-1996; 96US-0022125.

XX (CORR ) CORNELL RES FOUND INC.

XX Bander NH;

XX WPI; 2000-571325/53.

XX N-PSDB; AAA37834.

DR

XX

PT Antibody specific for extracellular prostate-specific membrane antigen, useful for diagnosis and treatment of prostate cancer

PS Example 12; Column 22; 33pp; English.

XX This sequence is a fragment of the light chain of the monoclonal antibody J591. The invention relates to an isolated antibody or its antigen binding portion (I) which binds to an extracellular domain of prostate specific membrane antigen and which does not require cell lysis to bind to the extracellular domain. The antibody or its antigen binding portion is selected for its ability to bind to live cells. (I) is useful for diagnosis of diseases associated with the presence of normal, benign hyperplastic, and cancerous epithelial cells or portions. Also it can be used for identifying the recurrence of such diseases, particularly when the disease is localised in a particular biological material of the patient for e.g. recurrence of prostatic disease. They can also be used alone or bound to a substance effective to kill cancerous prostate epithelial cells as a therapy for prostate cancer. Binding and internalising of the antibody with the prostate specific membrane antigen, permits the therapeutic use of intracellularly acting cytotoxic agents. (I) targets only prostate epithelial cells and other tissue are spared which provides safer treatment particularly for elderly patients. The antibodies bind to living prostate cells and treatments using these antibodies are more effective than those which target lysed prostate cells.

SQ Sequence 107 AA;

Query Match 100.0%; Score 562; DB 21; Length 107;

Best Local Similarity 100.0%; Pred. No. 1.2e-39;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIWVTQSPKSMMSVGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60

DB 1 NIWMTQSPKSMMSVGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRVTGVPD 60

QY 61 RFTGSGSATDFTLTISVQAEADLYHCGGYSPYPTFGGGTKLEIK 107

DB 61 RFTGSGSATDFTLTISVQAEADLYHCGGYSPYPTFGGGTKLEIK 107

## RESULT 3

AAB10444

ID AAB10444 standard; protein; 107 AA.

AC AAB10444;

DT 01-DEC-2000 (first entry)

DE Murine monoclonal antibody MAK HE2 variable region light chain.

XX Murine; monoclonal antibody; MAK HE2; light chain; variable region;

KW human cellular membrane antigen; tumor associated antigen; TAA;

XX Mus sp.

XX WO200041722-A1.

XX 20-JUL-2000.

XX 12-JAN-2000; 2000WO-EP00174.

XX 13-JAN-1999; 99CH-0000051.

XX (IGEN-) IGENEON GMBH.

XX Eckert H, Loibner H;

XX WPI; 2000-475956/41.

XX

PT Novel use of antibodies against human cellular membrane antigens for  
 XX vaccination against cancer -  
 PS Example 3; Page 47-48; 54pp; German.  
 XX This invention describes the novel use of an antibody targeted to a  
 CC human cellular membrane antigen, to manufacture a medicament to  
 CC prophylactically and/or therapeutically vaccinate against cancer.  
 CC The antibodies against tumor associated antigen (TAA) for prophylactic  
 CC and/or therapeutic vaccination against cancer may be used in low doses  
 CC (when compared to antibodies against TAA for passive immunotherapy),  
 CC typically less than 1 mg by injection. The antibodies also have a long  
 CC continual activity that directly induces immunity and their shelf life  
 CC is unlimited (fresh vaccination is always possible). This sequence  
 CC represents the murine monoclonal antibody MAK HE2 variable region light  
 CC chain fragment which is used in the method of the invention.  
 XX Sequence 107 AA;  
 SQ

Query Match 100.0%; Score 562; DB 21; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-39;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NIVMTQSPKSMVSGERVTLTKKASENVVTVSVYQOKPEQSPKLLIYGASNRVTGVPD 60  
 Db 1 NIVMTQSPKSMVSGERVTLTKKASENVVTVSVYQOKPEQSPKLLIYGASNRVTGVPD 60  
 Qy 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYPTFGGKTLEIK 107  
 Db 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYPTFGGKTLEIK 107

RESULT 4  
 AAB36225  
 ID AAB36225 standard; Protein; 107 AA.  
 AC AAB36225;  
 XX  
 DT 15-FEB-2001 (first entry)  
 XX  
 DE Monoclonal antibody J591 kappa light chain V region #1.  
 XX  
 KW Mouse; antibody; heavy chain; prostate cancer; biological agent.  
 XX  
 OS Mus sp.  
 XX  
 PN US6136311-A.  
 XX  
 PD 24-OCT-2000.  
 XX  
 PF 17-JUL-1997; 97US-0895914.  
 XX  
 PR 06-MAY-1996; 96US-0016976.  
 XX  
 PR 18-JUL-1996; 96US-0022125.  
 XX  
 PR 09-APR-1997; 97US-0838682.  
 XX  
 XX (CORR.) CORNELL RES FOUND INC.  
 XX  
 XX Bander NH;  
 PI  
 DR WPI: 2001-040234/05.  
 DR N-PSDB; AAC66544.  
 XX  
 XX Use of E99, a J415, a J533 or a J591 monoclonal antibodies for ablating  
 PT or killing cancerous, especially non-prostate, cells (e.g. breast  
 PT cancerous cells or cancerous cells of metastatic adenocarcinoma to the  
 PT liver) -  
 XX  
 XX Example 12; Column 25; 35pp; English.  
 PS  
 XX The present invention describes a method of killing cancer cells,  
 CC particularly prostate cancer cells, by directing a biological agent to  
 CC

CC the cells which then binds to a prostate specific membrane antigen and  
 CC causes the molecule to be internalised. The internalisation of the agent,  
 CC which may be bound to a drug or which may act to kill the cell alone,  
 CC then leads to the death of the cell. The present sequence forms  
 CC part of an antibody which may be used as the biological agent of the  
 CC invention. In addition to prostate cancer, the method can be used with  
 CC renal, urothelial, colon, renal, lung and breast cancer cells, and  
 CC cancerous cells of metastatic adenocarcinoma to the liver.  
 XX Sequence 107 AA;  
 SQ

Query Match 100.0%; Score 562; DB 22; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-39;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NIVMTQSPKSMVSGERVTLTKKASENVVTVSVYQOKPEQSPKLLIYGASNRVTGVPD 60  
 Db 1 NIVMTQSPKSMVSGERVTLTKKASENVVTVSVYQOKPEQSPKLLIYGASNRVTGVPD 60  
 Qy 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYPTFGGKTLEIK 107  
 Db 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYPTFGGKTLEIK 107

RESULT 5  
 AAR27144  
 ID AAR27144 standard; Protein; 109 AA.  
 XX  
 AC AAR27144;  
 XX  
 DT 20-MAY-1998 (first entry)  
 XX  
 DE lE6 kappa light chain variable region.  
 XX  
 KW Chimeric; heavy chain; variable region; monoclonal antibody;  
 KW lymphocyte function associated antigen-3; LFA-3; inflammation;  
 KW autoimmune disease; immunomodulation; systemic lupus erythematosus;  
 KW rheumatoid arthritis; thyroiditis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT domain 24..34  
 FT /note= "CDR1"  
 FT domain 50..56  
 FT /note= "CDR2"  
 FT domain 89..97  
 FT /note= "CDR3"  
 XX  
 PN EP503646-A.  
 XX  
 PD 16-SEP-1992.  
 XX  
 PR 12-MAR-1992; 92EP-0104318.  
 XX  
 PR 12-MAR-1991; 91US-0667975.  
 XX  
 XX (BIOJ ) BIOGEN INC.  
 XX  
 XX Chisholm PL, Sato VL, Wallner BP;  
 PI  
 DR WPI: 1992-309758/38.  
 DR N-PSDB; AAQ28653.  
 XX  
 XX Monoclonal antibodies active against lymphocyte function  
 PT associated antigen-3 - for treating inflammation and auto-immune  
 PT diseases, and for detecting LFA-3 protein in a sample  
 XX  
 XX Claim 19; Page 14; 30pp; English.  
 PS  
 XX Light and heavy chain variable region sequences were deduced from  
 CC the DNA sequences obtd. by PCR of DNA sequences obtd. from the  
 CC



CC the disease is localised in a particular biological material of the  
CC patient for e.g. recurrence of prostatic disease. They can also be used  
CC alone or bound to a substance effective to kill cancerous prostate  
CC epithelial cells as a therapy for prostate cancer. Binding and  
CC internalising of the antibody with the prostate specific membrane  
CC antigen, permits the therapeutic use of intracellularly acting cytotoxic  
CC agents. (i) targets only prostate epithelial cells and other tissue are  
CC spared which provides safer treatment particularly for elderly patients.  
CC The antibodies bind to living prostate cells and treatments using these  
CC antibodies are more effective than those which target lysed prostate  
CC cells.

XX SQ Sequence 121 AA;

Query Match 100.0%; Score 562; DB 21; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.4e-39;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NIVMTQSPKSMMSVGERVTLTKASENVTVVSWYQOKPEQSPKLLIYGASNRVTGVPD 60  
Db 7 NIVMTQSPKSMMSVGERVTLTKASENVTVVSWYQOKPEQSPKLLIYGASNRVTGVPD 66  
Qy 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGSYPYTFGGGTKLEIK 107  
Db 67 RFTGSGSATDFTLTISVQAEADLADYHCGQGSYPYTFGGGTKLEIK 113

RESULT 8  
AAB36222  
ID AAB36222 standard; Protein; 121 AA.  
XX  
AC AAB36222;  
XX  
DT 15-FEB-2001 (first entry)  
XX  
DE Murine monoclonal antibody J591 kappa light chain #1.  
XX  
KW Mouse; antibody; heavy chain; prostate cancer; biological agent.

XX OS Mus sp.  
XX  
PN US6136311-A.  
XX  
PD 24-OCT-2000.  
XX  
PF 17-JUL-1997; 97US-0895914.  
XX  
PR 06-MAY-1996; 96US-0016976.  
PR 18-JUL-1996; 96US-0022125.  
PR 09-APR-1997; 97US-0838682.  
XX  
PA (CORR ) CORNELL RES FOUND INC.  
XX  
PI Bander NH;  
XX  
DR WPI: 2001-040234/05.  
DR N-PSDB; AAC66542.  
XX  
PT Use of E99, a J415, a J533 or a J591 monoclonal antibodies for ablating  
PT or killing cancerous, especially non-prostate, cells (e.g. breast  
PT cancerous cells or cancerous cells of metastatic adenocarcinoma to the  
PT liver) -  
XX  
PS Example 12; Fig 10; 35pp; English.

XX The present invention describes a method of killing cancer cells,  
CC particularly prostate cancer cells, by directing a biological agent to  
CC the cells which then binds to a prostate specific membrane antigen and  
CC causes the molecule to be internalised. The internalisation of the agent,  
CC which may be bound to a drug or which may act to kill the cell alone,  
CC then leads to the death of the cell. The present sequence forms  
CC part of an antibody which may be used as the biological agent of the

CC invention. In addition to prostate cancer, the method can be used with  
CC renal, urothelial, colon, renal, lung and breast cancer cells, and  
CC cancerous cells of metastatic adenocarcinoma to the liver.

XX SQ Sequence 121 AA;

Query Match 100.0%; Score 562; DB 22; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.4e-39;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NIVMTQSPKSMMSVGERVTLTKASENVTVVSWYQOKPEQSPKLLIYGASNRVTGVPD 60  
Db 7 NIVMTQSPKSMMSVGERVTLTKASENVTVVSWYQOKPEQSPKLLIYGASNRVTGVPD 66  
Qy 61 RFTGSGSATDFTLTISVQAEADLADYHCGQGSYPYTFGGGTKLEIK 107  
Db 67 RFTGSGSATDFTLTISVQAEADLADYHCGQGSYPYTFGGGTKLEIK 113

RESULT 9  
AAW01145  
ID AAW01145 standard; Protein; 127 AA.  
XX  
AC AAW01145;  
XX  
DT 10-FEB-1997 (first entry)  
XX  
DE MAb 10.1 light chain, directed against type II phospholipase A2.  
XX  
KW Monoclonal antibody; phospholipase; myocardial infarction;  
KW pancreatitis; cerebral infarction; acute kidney failure; colitis;  
KW chronic rheumatism; adult respiratory distress syndrome;  
KW cardiac shock; treatment; preclinical testing; disease; hybridoma.

XX OS Mus musculus.

XX  
FH Key Location/Qualifiers  
FT Binding-site 44..54  
FT /label= CDR 1  
FT Binding-site 70..76  
FT /label= CDR 2  
FT Binding-site 109..117  
FT /label= CDR 3

XX WO9620959-A1.  
XX  
XX 11-JUL-1996.  
XX  
XX 27-DEC-1995; 95WO-JP02714.  
XX  
XX 29-DEC-1994; 94JP-0340006.

(YAMA ) YAMANOUCHI PHARM CO LTD.

Kawauchi Y, Masuho Y, Takasaki J, Yasunaga T;

WPI: 1996-333946/33.  
N-PSDB; AAT40805.

Monoclonal antibody inhibiting type II phospholipase A2 activity  
for treatment of myocardial and cerebral infarction

Claim 6; Figure 13; 69pp; Japanese.

XX Monoclonal antibodies which inhibit type II phospholipase A2 are  
CC useful in the treatment of myocardial infarction, cerebral  
CC infarction, acute kidney failure, chronic rheumatism, cardiac shock,  
CC pancreatitis, adult respiratory distress syndrome and colitis. The  
CC antibodies were generated by immunising Balb/C mice with recombinant  
CC human type II phospholipase A2. Spleen cells from the mice were  
CC fused with mouse myeloma P3U1 (P3x63Ag8.U1) and the hybridomas  
CC obtained were screened for phospholipase A2 inhibitory activity.

CC Active clones were isolated including 12H5, 1.4 and 10.1. These  
 CC were cultured and the antibody isolated from the culture  
 CC supernatant by precipitation with ammonium sulphate and purification  
 CC on a column of protein A-Sepharose CL4B. Because the antibody acts  
 CC on the primate and mouse forms of enzyme as well as human it is  
 CC particularly suitable for preclinical testing.

XX Sequence 127 AA;

Query Match 100.0%; Score 562; DB 17; Length 127;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-39;  
 Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMSSVGERVTLTKCKASENVVTVSWYQKPEQSPKLLIYGASNRVTGVPD 60  
 |||||  
 Db 21 NIVMTQSPKSMSSVGERVTLTKCKASENVVTVSWYQKPEQSPKLLIYGASNRVTGVPD 80  
 |||||  
 QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYPTFGGKLEIK 107  
 |||||  
 Db 81 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYPTFGGKLEIK 127  
 |||||

# RESULT 10

AAW01632  
 ID AAW01632 standard; Protein; 136 AA.

AC AAW01632;

DT 22-JUL-1997 (first entry)

XX Ber-H2 heavy kappa chain.

DE CD30; immunoglobulin; variable region; CDR; cancer; diagnosis;  
 KW therapy; Ber-H2.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide

FT 1..29

FT /label= sig\_peptide

FT Protein

FT 30..136

FT /label= mat\_protein

XX DE19543039-C1.

XX 21-NOV-1996.

XX 08-NOV-1995; 95DE-1043039.

XX 08-NOV-1995; 95DE-1043039.

XX (MEDA-) MEDAC GES KLINISCHE SPEZIALPRAEPARATE.  
 XX Stein H, Ziegler A;

XX WPI; 1996-507017/51.

XX N-PSDB; AAT58329.

XX DNA mols. encoding CD30-specific immunoglobulin variable regions -  
 PT useful for cancer diagnosis or therapy  
 XX Claim 15; Page 15; 20pp; German.

XX The ligands are useful for diagnosis or therapy of CD30 expressing  
 CC cancers, esp. Hodgkinson's disease.  
 CC Cytoplasmic RNA was isolated from cells of the mouse myeloma

CC hybrid line Ber-H2. cDNA was isolated using reverse transcriptase.  
 CC A VHDJ fragment contg. band was cut from a gel and purified. DNA  
 CC corresponding to VK and Vgamma was isolated and cloned into  
 CC vectors. Oligonucleotides used are given in AAT58331 to AAT58340.

XX Sequence 136 AA;

Query Match 93.8%; Score 527; DB 17; Length 136;  
 Best Local Similarity 94.4%; Pred. No. 1.2e-36;  
 Matches 101; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 NIVMTQSPKSMSSVGERVTLTKCKASENVVTVSWYQKPEQSPKLLIYGASNRVTGVPD 60  
 |||||  
 Db 30 NIVMTQSPKSMSSVGERVTLTKCKASENVVTVSWYQKPEQSPKLLIYGASNRVTGVPD 89  
 |||||

QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYPTFGGKLEIK 107  
 |||||  
 Db 90 RFTGSGSATDFTLTISVQAEDLADYHCGQGYSPYPTFGGKLEIK 136  
 |||||

# RESULT 11

AA71545  
 ID AAY71545 standard; Protein; 127 AA.

AC AAY71545;

DT 12-OCT-2000 (first entry)

XX Mouse AF2 antibody light chain variable region (AF2-VL).

XX Humanised antibody; HuZAF; mouse AF2 antibody; human EU antibody; AF2-VL;  
 KW light chain variable region; VL; heavy chain variable region; VH; IgG2b;  
 KW gamma-interferon; IFN; complementarity determining region; CDR; FR;  
 KW framework region; immunosuppressive; antiinflammatory; antisclerotic;  
 KW gastrointestinal; antidiabetic; antiarthritic; dermatological; inhibitor;  
 KW autoimmune disease; graft versus host disease; organ transplant;  
 KW multiple sclerosis; Type I diabetes; rheumatoid arthritis; psoriasis;  
 KW systemic lupus erythematosus; SLE; Crohn's disease.

XX Mus sp.

XX Key Location/Qualifiers

FT Peptide

FT 1..20

FT /note= "N-terminal peptide"

FT Protein

FT 21..127

FT /note= "Mature mouse antibody AF2 light chain variable  
 region (AF2-VL)"

FT Region

FT 44..54

FT /label= CDR

FT /note= "Complementarity determining region"

FT Region

FT 70..76

FT /label= CDR

FT /note= "Complementarity determining region"

FT Region

FT 109..117

FT /label= CDR

FT /note= "Complementarity determining region"

XX WO200032634-A1.

XX 08-JUN-2000.

XX 29-NOV-1999; 99WO-US28195.

XX 01-DEC-1998; 98US-0110523.

XX (PROT-) PROTEIN DESIGN LABS INC.

XX Vasquez M, Landolfi NF, Tsurushita N, Queen CL;

XX WPI; 2000-412292/35.

XX N-PSDB; AAD01345.

XX Humanized murine AF2 immunoglobulins, useful for inhibiting  
 PT gamma-interferon for the treatment of autoimmune diseases, e.g.  
 PT multiple sclerosis and diabetes -

XX Claim 1; Fig 1A; 32pp; English.

XX

The present amino acid sequence is the mouse AF2 antibody, light chain variable region (AF2-VL). It has IgG2b isotype and kappa light chain. It is used for the construction of humanised version of mouse AF2 antibody HuzAF, that comprises mouse antibody AF2 complementarity determining regions (CDRs), functionally joined to the human acceptor antibody Eu framework region (FR). HuzAF antibody specifically binds to and neutralises gamma-interferon (IFN). They can also block the binding of mouse AF2 immunoglobulin to gamma-IFN. HuzAF does not contain sequences that are immunogenically active in humans and remains unaffected by immune responses, that may reduce its activity or circulating half-life. HuzAF may be administered to treat autoimmune diseases such as graft versus host disease following organ transplant, type I diabetes, multiple sclerosis, rheumatoid arthritis, psoriasis, systemic lupus erythematosus (SLE), Hashimoto's thyroiditis, primary biliary cirrhosis and inflammatory bowel disease like, Crohn's disease.

SQ	Sequence	127 AA;
Query Match	92.7%	Score 521; DB 21; Length 127;
Best Local Similarity	91.6%	Pred. No. 3.6e-36;
Matches 98:	Conservative	5; Mismatches 4; Indels 0; Gaps 0;

QY	1	NIVMTSPKSMSSVGERVTU	TCKASENVNVTYSWYQOKPEQSPKLLIYGASNRRTGYVPD	60
		:	: : : : : :	
Db	21	nivmtgspksmyalgervtl	tsckasenvdtyvswyqkpeqspklliygasnrtygpd	80
		:	: : : : : :	
QY	61	RFTGSGSATDFTLISSVAQEDLADYHCQGYSYPYTFGGGTKEIK	107	
		:	: : : : : :	
Db	81	rftgsqsatdfllissvqaesladychcqgvnypfftgsatkktleik	127	
		:	: : : : : :	

RESULT 12  
AAB69693  
ID AAB69693 standard; Protein; 136 AA.  
XX  
XX  
AC AAB69693;  
XX  
XX  
DT 30-APR-2001 (first entry)  
XX  
XX  
DE Murine AF2 antibody light chain SEO ID NO: 99.

Humanised immunoglobulin; mouse; human; antibody; heavy chain; diabetes; light chain; graft versus host disease; transplant; autoimmune disease; multiple sclerosis; rheumatoid arthritis; systemic lupus erythematosus; myasthenia gravis; herpes infection; myeloid leukaemia; CMV infection.

XX	Mus sp.	
XX	US6180370-BI.	
PN		
XX	30-JAN-2001.	
PD		
XX		
PF	07-JUN-1995;	95US-0484537.
XX		
PR	28-DEC-1988;	88US-0290975.
PR	13-FEB-1989;	89US-0310252.
PR	28-SEP-1990;	90US-0590274.
PR	19-DEC-1990;	90US-0634278.

XX (PROT-) PROTEIN DESIGN LABS INC.  
PA  
XX  
XX  
PI Queen CL, Selick HE;  
XX  
XX WPI; 2001-190856/19.  
DR N-PSDB; AAF58757.  
DR

Producing humanized immunoglobulin, involves producing a cell containing DNA segments encoding humanized heavy and light chain variable regions and expressing the DNA segments in the cell -

PS Example 9; Fig 43; 145pp; English.

The present invention describes a method of producing humanised immunoglobulins involving expressing in a cell a nucleic acid encoding a humanised version of an immunoglobulin. This is obtained by comparing a donor and human immunoglobulin and producing a combined antibody which contains part of each. These are useful in the treatment of graft-versus-host disease, transplant rejection, autoimmune diseases such as diabetes, rheumatoid arthritis, myasthenia gravis, multiple sclerosis and systemic lupus erythematosus, herpes infections, CMV virus infections and myeloid leukaemia. The present sequence is an antibody used to demonstrate the method of the invention.

AA	Sequence	136 AA;
SQ	Sequence	136 AA;

Query Match	92.7%;	Score 521;	DB 22;	Length 136;
Best Local Similarity	91.6%;	Pred. NO. 3.9e-36;		
Matches 98; Conservative	5;	Mismatches 4;	Indels 0;	Gaps 0;

QY	1	NIVMTQSPKSMGMSVGERVTTTC	KASENVTVYSWYQOKPEQSPKLLIYGASNRRTGVPD	60
Db	30	nivmtqspkmsyigervtlsc	kasenvtvsywgqkpeqspklllygasnrytgvpd	89
QY	61	RTGTGSATDFLTITSSVQAEDLADYH	CGQCYSPYFPGGTGLEIK	107
Db	90	rfkasgatdfiltissvqaedadvh	caqcyvpyffgsgtgleik	136

RESULT 13  
AAW00828  
ID AAW00828 standard; Protein; 108 AA.

XX	AAW00828;
AC	
XX	
DT	19-MAY-1997 (first entry)
XX	
DE	Variable light chain of anti-human Fas ligand antibody NOK-3
XX	
KW	Variable region; light chain; human; Fas ligand; monoclonal;
KW	antibody; NOK-3; hybridoma; inhibition; apoptosis; assay;
KW	diagnosis; disease; hepatitis; infectious mononucleosis;
KW	systemic lupus erythematosus; ss.

XX  
OS  
Mus musculus.

XX PN WO9629350-A1

XX  
PD 26-SEP-1996XX  
PF 21-MAR-1996XX  
27-OCT-1995: 95.TP-0303492

PR 20-MAR-1995; 95JP-0087420.  
XX

PA (SUME ) SUMITOMO ELECTRIC IN  
XX

PI Kayagaki N, Nakata M, Okumura K, Yagita H;  
yy

DR WPI; 1996-443140/44.  
DR N-DCDR. 88030554

XX

PT for the detection of Fas ligands either on cell surface or in PT solution

PS Claim 24; Pages 99-100; 133pp; Japanese.

The present sequence is the light chain variable region of the anti-human Fas ligand monoclonal antibody (MAB) NOK-3. NOK-3 is produced by the hybridoma NOK-3 (FERM BP-5046), which was prepared by immunising mice with transformed human Fas ligand expressing COS cells, and fusing spleen cells isolated from the mice with myeloma P3x63Ag8.653 (ATCC CRL-1580) cells. The MAB recognises the human Fas ligand on the cell surface or in solution, and can be used to

CC inhibit the apoptosis inducing cell surface Fas ligand/Fas  
 CC reaction. The Mab can also be used for a Fas ligand assay in  
 CC biological samples (e.g. human blood), especially for disease  
 CC diagnosis, e.g. hepatitis, infectious mononucleosis and systemic  
 CC lupus erythematosus.  
 XX  
 SQ Sequence 108 AA;

Query Match 90.6%; Score 509; DB 17; Length 108;  
 Best Local Similarity 90.7%; Pred. No. 3e-35;  
 Matches 97; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

QY 1 NIWMTQSPKMSMSGVGVTVTLTKASENVVTVSWYQQRPEQSPKLLIYGASNRVTGVPD 60

Db 1 NIWMTQSPKMSMSGVGVTVTLTKASENVVTVSWYQQRPEQSPKLLIYGASNRVTGVPD 60

QY 61 RFTGSGSATDFTLTISVQAEADLYHCGGYSYPYTFGGGTTKLEIK 107

Db 61 RFTGSGSATDFTLTISVQAEADLYHCGGYSYPYTFGGGTTKLEIK 107

# RESULT 14

AAR64812  
 ID AAR64812 standard; Protein; 239 AA.

XX AC AAR64812;

DT 15-JUL-1995 (first entry)

XX DE ScFv anti-HCG.

XX KW ScFv: single chain Fv; HCG: human chorionic gonadotropin;  
 KW Aspergillus; Mucor; Neurospora; Penicillium; PUR4138;  
 KW monoclonal antibody; Clearblue; fusion protein;  
 KW antibody engineering.

XX OS Mus sp.

FH Key Location/Qualifiers

FT Region 1..119 /label= VH  
 FT /note= "Mab Clearblue VH region"

FT Region 28..32 /label= CDRI

FT /note= "complementarity determining region 1"

FT Region 47..63 /label= CDRII

FT /note= "complementarity determining region 2"

FT Region 96..108 /label= CDRIII

FT /note= "complementarity determining region 3"

FT Region 120..134 /label= Linker

FT /note= "linker connecting the VH and VL regions"

FT Region 135..239 /label= VL

FT /note= "Mab Clearblue VL region"

FT Region 159..168 /label= CDRI

FT /note= "complementarity determining region 1"

FT Region 184..190 /label= CDRII

FT /note= "complementarity determining region 2"

FT Region 223..230 /label= CDRIII

FT /note= "complementarity determining region 3"

FT Peptide 275..285 /label= Myc\_tail

XX W09429457-A.

XX 22-DEC-1994.

XX

XX 09-JUN-1994; 94WO-EP01906.

XX 09-JUN-1993; 93EP-0201660.

PR 09-JUN-1993; 93EP-0201661.

PR 14-JUN-1993; 93EP-0201706.

XX (NEDE ) NEDERLAND ORG TNO.

PA (UNIL ) UNILEVER NV.

PA (UNIL ) UNILEVER PLC.

XX Freken LGJ, Hessing JGM, Musters W;

PI Vangorcor RFM, Verbakel JMA, Verrips CT, Van Den Hondel CAMJJ;

XX WPI: 1995-036484/05.

DR N-PSDB; AAQ76275.

XX Prodn. of single chain Fv antibody fragments - as fusion proteins

PT using a transformed mould of the genus Aspergillus, Mucor,

PT Neurospora or Penicillium

XX Example 1; Page 13-14; 70pp; English.

PS The PstI-XhoI fragment (given in AAQ76275) of PUR4138 encodes

CC the SCFv fragment (AAR64812) of anti-HCG monoclonal antibody

CC Clearblue.

XX Sequence 239 AA;

Query Match 85.8%; Score 482; DB 16; Length 239;

Best Local Similarity 85.7%; Pred. No. 1.1e-32;

Matches 90; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 NIWMTQSPKMSMSGVGVTVTLTKASENVVTVSWYQQRPEQSPKLLIYGASNRVTGVPD 60

Db 135 dieltgspkmsmsgvgtltsckasetvdfsvwygqkpegsplifgnsrfgvdp 194

QY 61 RFTGSGSATDFTLTISVQAEADLYHCGGYSYPYTFGGGTTKLE 105

Db 195 rftgsgsatdftltisvqaedfadyhcgqtnmpytfggggtkle 239

# RESULT 15

AAW21939

ID AAW21939 standard; Protein; 107 AA.

XX AC AAW21939;

XX 10-FEB-1998 (first entry)

XX Variable light subunit variant 4 of humanised murine antibody 24-31.

XX Variable light sequence; murine antibody 24-31; gp39; humoral immunity;

XX activated CD4+ T cell; B cell proliferation; immunodeficiency disease;

XX human V-kappa subgroup I; DEN; germline 012; rheumatoid arthritis;

XX multiple sclerosis; diabetes; systemic lupus erythematosus; ITP.

XX Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX W09717446-A2.

XX 15-MAY-1997.

XX 07-NOV-1996; 96WO-US17875.

XX 07-NOV-1995; 95US-0554840.

XX (IDEC-) IDEC PHARM CORP.

XX Black A, Hanna N, Newman RA, Padlan EA;

XX





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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2001, 09:01:39 ; Search time 25.84 Seconds  
(without alignments)  
315.429 Million cell updates/sec

Title: US-09-889-300A-2  
Perfect score: 562  
Sequence: 1 NIVMTQSPKSMMSVGERVT.....CGOGYSPYTFGGGKLEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	562	100.0	136	1 KVM521	Ig kappa chain pre
2	551	98.0	111	2 D37266	Ig kappa chain v r
3	515	91.6	107	2 S33132	Ig kappa chain v r
4	498	88.6	118	2 I33932	Ig kappa chain pre
5	494	87.9	107	2 S38713	Ig light chain v r
6	459	81.7	107	2 PL0268	Ig kappa chain v r
7	454	80.8	96	2 PH1070	Ig light chain v r
8	446.5	79.4	91	2 PH1071	Ig light chain v r
9	440	78.3	108	2 PL0204	anti-DNA autoantib
10	432	76.9	107	2 S32192	Ig kappa chain v r
11	429	76.3	117	2 S42466	Ig kappa chain v r
12	427	76.0	107	2 S32191	Ig kappa chain v r
13	422	75.1	149	1 KVM511	Ig kappa chain pre
14	419	74.6	127	2 S04577	Ig kappa chain pre
15	416	74.0	119	2 P00265	Ig kappa chain v r
16	410	73.0	107	2 A28195	Ig kappa chain v r
17	410	73.0	214	2 S68212	Ig kappa chain (Ma
18	409	72.8	152	2 S30751	Ig kappa chain pre
19	407	72.4	113	2 H30534	Ig kappa chain v r
20	407	72.4	131	2 PL0207	anti-Idiotypic ant
21	404	71.9	113	2 F30534	Ig kappa chain v r
22	403	71.7	114	1 KVM57A	Ig kappa chain v r
23	403	71.7	135	2 S38807	Ig light chain v-J
24	401	71.4	113	2 PL0264	Ig kappa chain v r
25	398.5	70.9	225	2 S37484	Ig kappa chain - m
26	396	70.5	128	2 A47159	Ig lambda chain v
27	395	70.3	107	2 D53285	Ig kappa chain v a
28	395	70.3	112	2 E30538	Ig kappa chain v r
29	395	70.3	112	2 F30538	Ig kappa chain v r

30	394	70.1	107	2 B28195	Ig kappa chain v r
31	394	70.1	113	2 JC2270	PL7-6 antibody lig
32	393	69.9	109	2 S26336	Ig light chain v r
33	392	69.8	100	2 H38601	Ig kappa chain v r
34	392	69.8	113	2 PL0263	Ig kappa chain v r
35	391	69.6	134	2 PC1214	Ig kappa chain pre
36	389.5	69.3	108	2 PL0083	Ig kappa chain v r
37	389	69.2	129	2 S52793	Ig kappa chain v r
38	388.5	69.1	118	2 PT0356	Ig kappa chain v r
39	387	68.9	108	2 B49047	Ig kappa chain v r
40	385	68.5	129	2 S40317	Ig kappa chain - h
41	384	68.3	109	2 S31981	Ig kappa chain - h
42	384	68.3	114	1 K4HULN	Ig kappa chain v-I
43	383	68.1	111	2 B37266	Ig kappa chain v r
44	382.5	68.1	112	2 S41393	Ig kappa chain v r
45	382.5	68.1	113	2 PT0407	Ig light chain v r

## ALIGNMENTS

RESULT 1

KVMS21  
Ig kappa chain precursor V region (MOPC 21) - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 31-Mar-1980 #sequence\_revision 02-Apr-1982 #text\_change 22-Jun-1999  
C:Accession: A93736; A90262; B49982; A01917  
R:Hamlyn, P.H.; Gait, M.J.; Milstein, C.  
Nucleic Acids Res. 9, 4485-4494, 1981  
A:Title: Complete sequence of an immunoglobulin mRNA using specific priming and the d  
A:Reference number: A93736; MUID:82059477  
A:Accession: A93736  
A:Molecule type: mRNA  
R:Residues: 1-136 <HAM>  
R:SVasti, J.; Milstein, C.  
Biochem. J. 128, 427-444, 1972  
A:Title: The complete amino acid sequence of a mouse kappa light chain.  
A:Reference number: A90262; MUID:73053310  
A:Contents: myeloma protein MOPC 21  
A:Accession: A90262  
A:Molecule type: protein  
A:Residues: 30-136 <SVA>  
R:Li, C.; Kiebel-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, J. Biol Chem 269 2805-2813 1994

A:Title: Topology of an antiferite-binding protein.

A:Reference number: A49982; MUID:94132051

A:Accession: B49982

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 30-136 <LIN>

A:Cross-references: GB:L24803; NID:g452098; PIDN:AAC37684.1; PID:g452099

A:Experimental source: clone BA7.1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:superfamily: immunoglobulin v region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-29/Domain: signal sequence #status predicted <STG>

F:30-136/Product: Ig kappa chain v region (MOPC 21) #status experimental <MAT>

F:45-119/Domain: immunoglobulin homology <IMM>

F:125-136/Region: J segment (JK2)

F:52-117/Disulfide bonds: #status predicted

Query Match 100.0%; Score 562; DB 1; Length 136;

Best Local Similarity 100.0%; Pred. No. 2.2e-42;

Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NIVMTQSPKSMMSVGERVTLTCKASENVVTVSVYQKPEQSPKLLIYGASNRVTGVPD 60

Db 30 NIVMTQSPKSMMSVGERVTLTCKASENVVTVSVYQKPEQSPKLLIYGASNRVTGVPD 89

Qy 61 RFTGSGSATDFTLTITSSVOAEDLADYHCGOGYSYPYTFGGGKLEIK 107

```
Db 90 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYPYTFGGGKLEIK 136
RESULT 2
Ig kappa chain V region (129) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C:Accession: D37266
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti
A:Reference number: A38740; MUID:91177923
A:Accession: D37266
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-111 <RUF>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-93/Domain: immunoglobulin homology <IMM>

Query Match 98.0%; Score 551; DB 2; Length 111;
Best Local Similarity 98.1%; Pred. No. 1.7e-41;
Matches 105; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 NIYVTSQPKSMSVSGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRYTGVPD 60
Db 4 DIVVTQIPKSMSSVSGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRYTGVPD 63
QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYPYTFGGGKLEIK 107
Db 64 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYPYTFGGGKLEIK 110

RESULT 3
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S33132
R:Tempest, P.R.; Barbanti, E.; Bremner, P.; Carr, F.J.; Ghislieri, M.; Rifaldi, B.; Marc
submitted to the EMBL Data Library, May 1993
A:Description: A humanized anti-tumor necrosis factor alpha monoclonal antibody that act
A:Reference number: S33131
A:Accession: S33132
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-107 <TEM>
C:Cross-references: EMBL:Z22670; NID:g297473; PIDN:CAA80379.1; PID:g297474
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 91.6%; Score 515; DB 2; Length 107;
Best Local Similarity 92.5%; Pred. No. 2.2e-38;
Matches 99; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 NIYVTSQPKSMSVSGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRYTGVPD 60
Db 1 NIYVTSQPKSMSVSGERVTLTCKASENVDTFVSWYQKPEQSPKLLIYGASNRYTGVPD 60
QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYPYTFGGGKLEIK 107
Db 61 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYIFPPTLGGGKLEIK 107

RESULT 4
I33932
Ig kappa chain precursor V region (E7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 21-Jan-2000

C:Accession: I33932
R:Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989
A:Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated ger
A:Reference number: A33932; MUID:89282823
A:Accession: I33932
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-118 <BAC>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:39-113/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 498; DB 2; Length 118;
Best Local Similarity 100.0%; Pred. No. 7.5e-37;
Matches 95; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NIYVTSQPKSMSVSGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRYTGVPD 60
Db 24 NIYVTSQPKSMSVSGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRYTGVPD 83
QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYP 95
Db 84 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYP 118

RESULT 5
S38713
Ig light chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000
C:Accession: S38713
R:Cimaniis, A.Y.
submitted to the EMBL Data Library, November 1993
A:Reference number: S38713
A:Accession: S38713
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <CIM>
C:Cross-references: EMBL:X76019; NID:g416090; PIDN:CAA53606.1; PID:g1333952
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 87.9%; Score 494; DB 2; Length 107;
Best Local Similarity 88.8%; Pred. No. 1.5e-36;
Matches 95; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 NIYVTSQPKSMSVSGERVTLTCKASENVVTVYVSWYQKPEQSPKLLIYGASNRYTGVPD 60
Db 1 DIVLTQSPKSMSSVSGERVTLTCKASENVDTYVSWYQKPEQSPKLLIYGASNRYTGVE 60
QY 61 RFTGSGSATDFTLTISVQAEDLADYHCGGYSYPYTFGGGKLEIK 107
Db 61 RFTGSGSATDFTLTISVQAEDLADYCGQSYSLPTFGAGTKLEK 107

RESULT 6
PL0268
Ig kappa chain V region (anti-DNA, DP9VK and DP17VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
C:Accession: PL0268
R:Shionochik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A:Reference number: PL0231; MUID:90111618
A:Accession: PL0268
A:Molecule type: mRNA
A:Residues: 1-107 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
```

C:Keywords: heterotetramer; immunoglobulin  
F:1-23/Region: framework 1  
F:16-90/Domain: immunoglobulin homology <IMM>  
F:24-34/Region: complementarity-determining 1  
F:35-49/Region: framework 2  
F:50-56/Region: complementarity-determining 2  
F:57-88/Region: framework 3  
F:89-97/Region: complementarity-determining 3  
F:98-107/Region: framework 4

Query Match 81.7%; Score 459; DB 2; Length 107;  
Best Local Similarity 82.2%; Pred. No. 1.7e-33;  
Matches 88; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

Qy 1 NIVMTQSPKSMMSGVGERVTLTKKASENVTVSVYQKPEQSPKLLIYGASNRVTGVPD 60  
Db 1 NIVMAWSPKSMMSGVGERVTLTKKASENVTVSVYQQTPEQSPKLLIYRASDRYFGVPD 60

Qy 61 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYPTFGGKLEIK 107  
Db 61 RFAGSGSAADFTLTSSVHAEDLADYCEQSYNYPTWTFGGGKLEVK 107

RESULT 7  
Ph1070  
Ig light chain V region (clone 17s 5) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PH1070  
J. Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.  
R. Exp. Med. 176, 761-779, 1992  
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells  
A:Reference number: PH0971; MUID:92381444  
A:Accession: PH1070  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-96 <TIL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 80.8%; Score 454; DB 2; Length 96;  
Best Local Similarity 93.9%; Pred. No. 4.2e-33;  
Matches 92; Conservative 1; Mismatches 3; Indels 2; Gaps 2;

Qy 1 NIVMTQSPKSMMSGVGERVTLTKKASENVTVSVYQKPEQSPKLLIYGASNRVTGVPD 60  
Db 1 NIVMTQSPKSMMSGVGERVTLTKKASENVTVSVYQKPEQSPKLLIYGASNRVTGVPD 60

Qy 61 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYPTFG 98  
Db 61 RFTGSGSATDFTLTSSVQAEADLADYHCGQ-YS-PRTF 96

RESULT 8  
Ph1071  
Ig light chain V region (clone 165.3m) - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 21-Jan-2000  
C:Accession: PH1071  
J. Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.  
R. Exp. Med. 176, 761-779, 1992  
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cells  
A:Reference number: PH0971; MUID:92381444  
A:Accession: PH1071  
A:Status: nucleic acid sequence not shown  
A:Molecule type: mRNA  
A:Residues: 1-91 <TIL>  
A:Experimental source: B cell, strain [NZB x NZW]F1  
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin  
F:10-83/Domain: immunoglobulin homology <IMM>

Query Match 79.4%; Score 446.5; DB 2; Length 91;  
Best Local Similarity 93.5%; Pred. No. 1.8e-32;  
Matches 86; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

Qy 7 SPKSMMSGVGERVTLTKKASENVTVSVYQKPEQSPKLLIYGASNRVTGVPDRFTGSG 66  
Db 1 SPKSMMSGVGERVTLTKKASENVTVSVYQKPEQSPKLLIYGASNRVTGVPDRFTGSG 59

Qy 67 SATDFTLTSSVQAEADLADYHCGQGYSPYPTF 98  
Db 60 SATDFTLTSSVQAEADLADYHCGQSYSPYPTF 91

RESULT 9  
PL0204  
anti-DNA autoantibody BV17-45, kappa chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: PL0204  
R. Smith, R.G.; Voss Jr., E.W.  
Mol. Immunol. 27, 463-470, 1990  
A:Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from BALB/c mice  
A:Reference number: PL0198; MUID:90309768  
A:Accession: PL0204  
A:Molecule type: mRNA  
A:Residues: 1-108 <SMI>  
A:Cross-references: GB:X53644; NID:q50198; PIDN:CAA37695.1; PID:q930144  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>  
F:24-34/Region: complementarity-determining 1  
F:50-56/Region: complementarity-determining 2  
F:89-97/Region: complementarity-determining 3  
F:96-108/Region: JH region

Query Match 78.3%; Score 440; DB 2; Length 108;  
Best Local Similarity 79.4%; Pred. No. 7.9e-32;  
Matches 85; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

Qy 1 NIVMTQSPKSMMSGVGERVTLTKKASENVTVSVYQKPEQSPKLLIYGASNRVTGVPD 60  
Db 1 DIVMTQSPKSMMSGVGERVTLTKKASENVTVSVYQKPEQSPKLLIYGASNRVTGVPD 60

Qy 61 RFTGSGSATDFTLTSSVQAEADLADYHCGQGYSPYPTFGGKLEIK 107  
Db 61 RFTGSGSGTDFTLTSSVQSEADLAEYFCQYNSYPYPTFGGKLEIK 107

RESULT 10  
S32192  
Ig kappa chain V region - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C:Date: 06-Feb-1995 #sequence\_revision 06-Feb-1995 #text\_change 21-Jan-2000  
C:Accession: S32192  
R. Izui, S.  
submitted to the EMBL Data Library, February 1993  
A:Reference number: S32185  
A:Accession: S32192  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-107 <IZU>  
A:Cross-references: EMBL:X70097; NID:288262; PIDN:CAA49701.1; PID:q288263  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 432; DB 2; Length 107;  
Best Local Similarity 79.4%; Pred. No. 3.9e-31;

```
Matches 85; Conservative 8; Mismatches 14; Indels 0; Gaps 0;

QY 1 NIYMTQSPKSMMSGVGERVTLTKKASENVVTVSWYQQRPEQSPKLLIYGASNRVTGVPD 60
:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 DIVMTQSHKFMSTSVGDRVSIITCKASQDVSTAVAWYQQRPGQSPKLLIYSASRYTGVDP 60
:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 RFTGSGSATDFTLTSSVQAEDLADYHCQGYSPYPTFGGGTKLEIK 107
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 RFTGSGSGTDFTTISSVQAEDLAVYVCOQHYSPTPTFGGGTKLEIK 107
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
S42466
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42466
R:Shiyanov, P.A.; Bessalov, I.A.; Terletskaya, H.N.; Deyev, S.M.
submitted to the EMBL Data Library, March 1994
A:Reference number: S42466
A:Accession: S42466
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-117 <SHI>
A:Cross-references: EMBL:X78108; NID:g460824; PIDN:CAA54998.1; PID:g460825
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-100/Domain: immunoglobulin homology <IMM>

Query Match 76.3%; Score 429; DB 2; Length 117;
Best Local Similarity 78.5%; Pred. No. 7.8e-31;
Matches 84; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

QY 1 NIYMTQSPKSMMSGVGERVTLTKKASENVVTVSWYQQRPEQSPKLLIYGASNRVTGVPD 60
:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 11 DIVMTQSHKFMSTSVGDRVSIITCKASQDVSTAVAWYQQRPGQSPKLLIYWASRHTGVDP 70
:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 RFTGSGSATDFTLTSSVQAEDLADYHCQGYSPYPTFGGGTKLEIK 107
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 71 RFTGSGSGTDFLTITSNVQSEDLADYFCQOYSSYPYPTFGGGTKLEIK 117
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 12
S32191
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 21-Jan-2000
C:Accession: S32191
R:Izui, S.
submitted to the EMBL Data Library, February 1993
A:Reference number: S32185
A:Accession: S32191
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <Tzu>
A:Cross-references: EMBL:X70095; NID:g288260; PIDN:CAA49700.1; PID:g288261
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 76.0%; Score 427; DB 2; Length 107;
Best Local Similarity 78.5%; Pred. No. 1.1e-30;
Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 NIYMTQSPKSMMSGVGERVTLTKKASENVVTVSWYQQRPEQSPKLLIYGASNRVTGVPD 60
:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 DIVMTQSHKFMSTSVGDRVSIITCKASQDVSTAVAWYQQRPGQSPKLLIYSASRYTGVDP 60
:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 RFTGSGSATDFTLTSSVQAEDLADYHCQGYSPYPTFGGGTKLEIK 107
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 RFTGSGSGTDFTTISSVQPEDLAVYVCOQHYSPTPTFGGGTKLEIK 107
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 13
KVMS11
Ig kappa chain precursor V region (MPC11) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-Feb-1984 #sequence_revision 19-Feb-1984 #text_change 21-Jan-2000
C:Accession: A90823; A90753; A90298; A01916
R:Kelley, D.E.; Coleclough, C.; Perry, R.P.
Cell 29, 681-689, 1982
A:Title: Functional significance and evolutionary development of the 5'-terminal regi
A:Reference number: A90823; MUID:83001944
A:Accession: A90823
A:Molecule type: DNA
A:Residues: 1-71 <REL>
A>Note: The sequence was determined from the differentiated gene
R:Rabbits, T.H.; Hamlyn, P.H.; Matthysens, G.; Roe, B.A.
Can. J. Biochem. 58, 176-187, 1980
A:Title: The variability, arrangement, and rearrangement of immunoglobulin genes.
A:Reference number: A90753; MUID:80176554
A:Accession: A90753
A:Molecule type: mRNA
A:Residues: 41-149 <RAB>
R:Smith, G.P.
Biochem. J. 171, 337-347, 1978
A:Title: Sequence of the full-length immunoglobulin kappa-chain of mouse myeloma MPC
A:Reference number: A90298; MUID:78186617
A:Contents: myeloma protein MPC11
A:Accession: A90298
A:Molecule type: protein
A:Residues: 30-149 <SMI>
A>Note: The amidation states of residues 58, 69, 101, 111, 120, 122, and 123 were not
C:Comment: The mature chain has 12 additional residues at its amino end, due to a tan
42 corresponds to the amino-terminal residue of typical kappa chains.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: duplication; heterotetramer; immunoglobulin
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-149/Product: Ig kappa chain V region (MPC11) #status experimental <MAT>
F:57-131/Domain: immunoglobulin homology <IMM>
F:64-129/Disulfide bonds: #status predicted
```

```
Query Match 75.1%; Score 422; DB 1; Length 149;
Best Local Similarity 78.5%; Pred. No. 4e-30;
Matches 84; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 NIYMTQSPKSMMSGVGERVTLTKKASENVVTVSWYQQRPEQSPKLLIYGASNRVTGVPD 60
:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 42 DIVMTQSHKFMSTSVGDRVSIITCKASQDVSTTVAWYQQRPGQSPKLLIYSASRYTGVDP 101
:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 61 RFTGSGSATDFTLTSSVQAEDLADYHCQGYSPYPTFGGGTKLEIK 107
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 102 RFTGSGSGTDFTTISSVQAEDLAVYVCOQHYSPTPTFGGGTKLEIK 148
||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 14
S04577
Ig kappa chain precursor V region (MRL-RF28L) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: S04577
R:Kofler, R.; Duchosal, M.A.; Dixon, F.J.
submitted to the EMBL Data Library, March 1989
A:Description: Complexity, polymorphism and connectivity of murine V(kappa) gene fami
A:Reference number: S04577
A:Accession: S04577
A:Molecule type: mRNA
A:Residues: 1-127 <KOF>
A:Cross-references: EMBL:X14622; NID:g52400; PIDN:CAA32775.1; PID:g52401
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
```



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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2001, 09:03:06 ; Search time 22.67 seconds  
(without alignments)  
106.213 Million cell updates/sec

Title: US-09-889-300A-2  
Perfect score: 562  
Sequence: 1 NIVMTQSPKMSMSVGRVT.....CGQGYSPYPTFGGTKLEIK 107

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	562	100.0	107	3	US-08-838-682-16
2	562	100.0	107	4	US-08-895-914-16
3	562	100.0	107	4	US-09-357-710A-16
4	562	100.0	109	5	PCT-US92-02044-2
5	562	100.0	121	3	US-08-838-682-11
6	562	100.0	121	4	US-08-895-914-11
7	562	100.0	121	4	US-09-357-710A-11
8	521	92.7	136	1	US-07-634-278-99
9	521	92.7	136	1	US-08-477-728-99
10	521	92.7	136	1	US-08-474-040-99
11	521	92.7	136	1	US-08-487-200-99
12	521	92.7	136	4	US-08-484-537-99
13	454	80.8	107	3	US-08-554-840-4
14	449	79.9	107	3	US-08-554-840-2
15	447	79.5	107	3	US-08-554-840-3
16	444	79.0	107	3	US-08-554-840-1
17	441	78.5	107	1	US-07-634-278-103
18	441	78.5	107	1	US-08-477-728-103
19	441	78.5	107	1	US-08-474-040-103
20	441	78.5	107	1	US-08-487-200-103
21	441	78.5	107	4	US-08-484-537-103
22	426	75.8	108	4	US-09-157-370-4
23	424.5	75.5	108	2	US-08-657-012-25
24	424.5	75.5	108	3	US-09-013-872-25
25	424.5	75.5	108	4	US-09-184-198-25
26	424	75.4	249	2	US-08-797-689-18
27	423	75.3	108	4	US-08-752-693A-1

28	423	75.3	132	1	US-08-253-877C-55	Sequence 55, Appl
29	423	75.3	132	2	US-08-452-164A-55	Sequence 55, Appl
30	423	75.3	132	4	US-08-976-183A-36	Sequence 36, Appl
31	423	75.3	132	4	US-08-976-183A-37	Sequence 37, Appl
32	422	75.1	237	2	US-08-224-591-16	Sequence 16, Appl
33	422	75.1	237	2	US-08-926-789-16	Sequence 16, Appl
34	422	75.1	241	2	US-08-224-591-18	Sequence 18, Appl
35	422	75.1	241	2	US-08-926-789-18	Sequence 18, Appl
36	420	74.7	147	2	US-08-653-402B-4	Sequence 4, Appl
37	419	74.6	250	1	US-08-133-804-2	Sequence 2, Appl
38	419	74.6	250	1	US-08-461-184-8	Sequence 8, Appl
39	419	74.6	250	1	US-08-463-675-8	Sequence 8, Appl
40	419	74.6	250	1	US-08-464-589-8	Sequence 8, Appl
41	419	74.6	250	1	US-08-461-838-2	Sequence 2, Appl
42	419	74.6	250	2	US-08-461-386-2	Sequence 2, Appl
43	418.5	74.5	124	3	US-08-486-151-4	Sequence 4, Appl
44	416	74.0	106	2	US-08-822-830B-4	Sequence 4, Appl
45	416	74.0	106	2	US-08-950-660-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1  
US-08-838-682-16  
; Sequence 16, Application US/08838682  
; Patent No. 6107090  
; GENERAL INFORMATION:  
; APPLICANT: Gander M.D., Neil H.  
; TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE  
; TITLE OF INVENTION: CANCER  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
; STREET: Clinton Square, P.O. Box 1051  
; CITY: Rochester  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 14603-1051  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/838,682  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/016,976  
; FILING DATE: 06-MAY-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/022,125  
; FILING DATE: 18-JUL-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldman, Michael L.  
; REGISTRATION NUMBER: 30,727  
; REFERENCE/DOCKET NUMBER: 19603/1172  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (716) 263-1304  
; TELEFAX: (716) 263-1600  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-838-682-16

Query Match 100.0%; Score 562; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 1.7e-50;

Matches	107;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
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[illegible]

## RESULT 2

```

US-08-895-914-16
: Sequence 16, Application US/08895914
: Patent No. 6136311
: GENERAL INFORMATION:
: APPLICANT: Bander, Neil H.
: TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER
: NUMBER OF SEQUENCES: 19
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP
: STREET: Clinton Square, P.O. Box 1051
: CITY: Rochester
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 14603-1051
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/895,914

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Query Match 100.0%; Score 562; DB 4; Length 107;

Best Local Similarity	100.0%;	Pred. No. 1.7e-50;	
Matches 107;	Conservative	0;	Mismatches 0;
			Indels 0;
			Gaps 0;

[illegible]

### RESULT

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US-09-357-710A-16
; Sequence 16, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
; APPLICANT:  Bander,  Neil H.
; TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE:  Lois M. Kwasigroch; BZL 242/025
; CURRENT APPLICATION NUMBER:  US/09/357,710A
; CURRENT FILING DATE:  1999-07-20
; PRIOR APPLICATION NUMBER:  US 08/838,682
; PRIOR FILING DATE:  1997-04-09
; PRIOR APPLICATION NUMBER:  US 60/016,976
; PRIOR FILING DATE:  1996-05-06
; PRIOR APPLICATION NUMBER:  US 60/022,125
; PRIOR FILING DATE:  1996-07-18
; NUMBER OF SEQ ID NOS:  21
; SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 16
; LENGTH:  107
; TYPE:  PRT
; ORGANISM:  Mus sp.
; US-09-357-710A-16

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Query Match	Score 562;	DB 4;	Length 107;
100.00;			

Best Local Similarity	100.0%;	Pred. No. 1.7e-50;	
Matches 107;	Conservative	0;	Mismatches 0;
Indels			0;
Caps			0;

[illegible]

## RESULT

PCT-US92-02044-2  
; Sequence 2, Application PC/TUS9202044  
; GENERAL INFORMATION:  
; APPLICANT: BIOGEN, INC.  
; APPLICANT: SATO, Vicki L.  
; APPLICANT: CHISHOLM, Patricia L.  
; APPLICANT: WALLINER, Barbara P.  
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES RECOGNIZING  
; TITLE OF INVENTION: LYMPHOCYTE FUNCTION ASSOCIATED ANTIGEN-2  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: C/O FISH & NEAVE  
; STREET: 875 Third Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10022  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/02044  
; FILING DATE: 19920312  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/667,975  
; FILING DATE: 12-MAR-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: HALEY Jr., James F.  
; REGISTRATION NUMBER: 27,794  
; REFERENCE/DOCKET NUMBER: B150CIP

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 715-0600  
TELEFAX: (212) 715-0673  
TELEX: 14-8367  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 109 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US92-02044-2

Query Match 100.0%; Score 562; DB 5; Length 109;  
Best Local Similarity 100.0%; Pred. No. 1.7e-50;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 NIVMTQSPKSMMSGVGERVTLTKKASENVVTVSVWYQKPEQSPKLLIYGASNRVTGVPD 60  
Db 1 NIVMTQSPKSMMSGVGERVTLTKKASENVVTVSVWYQKPEQSPKLLIYGASNRVTGVPD 60  
Qy 61 RFTGSGSATDFTLTISSVQAEADLADYHCGQGYSYPYTFGGGTKLEIK 107  
Db 61 RFTGSGSATDFTLTISSVQAEADLADYHCGQGYSYPYTFGGGTKLEIK 107

RESULT 5  
US-08-838-682-11  
Sequence 11, Application US/08838682  
Patent No. 6107090  
GENERAL INFORMATION:  
APPLICANT: Bander M.D., Neil H.  
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF PROSTATE  
TITLE OF INVENTION: CANCER  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603-1051  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/838,682  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/016,976  
FILING DATE: 06-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/022,125  
FILING DATE: 18-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/1172  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-838-682-11

Query Match 100.0%; Score 562; DB 3; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.9e-50;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 NIVMTQSPKSMMSGVGERVTLTKKASENVVTVSVWYQKPEQSPKLLIYGASNRVTGVPD 60  
Db 7 NIVMTQSPKSMMSGVGERVTLTKKASENVVTVSVWYQKPEQSPKLLIYGASNRVTGVPD 66  
Qy 61 RFTGSGSATDFTLTISSVQAEADLADYHCGQGYSYPYTFGGGTKLEIK 107  
Db 67 RFTGSGSATDFTLTISSVQAEADLADYHCGQGYSYPYTFGGGTKLEIK 113

RESULT 6  
US-08-895-914-11  
Sequence 11, Application US/08895914  
Patent No. 6136311  
GENERAL INFORMATION:  
APPLICANT: Gardner, Neil H.  
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF CANCER  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603-1051  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/895,914  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/016,976  
FILING DATE: 06-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/022,125  
FILING DATE: 18-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/838,682  
FILING DATE: 09-APR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/1173  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 121 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-895-914-11

Query Match 100.0%; Score 562; DB 4; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.9e-50;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 NIVMTQSPKSMMSGVGERVTLTKKASENVVTVSVWYQKPEQSPKLLIYGASNRVTGVPD 60  
Db 7 NIVMTQSPKSMMSGVGERVTLTKKASENVVTVSVWYQKPEQSPKLLIYGASNRVTGVPD 66  
Qy 61 RFTGSGSATDFTLTISSVQAEADLADYHCGQGYSYPYTFGGGTKLEIK 107

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|||||
67  RFTGSGSATDFTLTSSVQAEADLADYHCGQGSYPYTFGGGPKLEIK 113

RESULT 7
US-09-357-710A-11
; Sequence 11, Application US/09357710A
; Patent No. 6290956
; GENERAL INFORMATION:
; APPLICANT:  Bandier, Neil H.
; TITLE OF INVENTION:  TREATMENT AND DIAGNOSIS OF PROSTATE CANCER
; FILE REFERENCE:  Lois M. Kwasigroch: BZL 242/025
; CURRENT APPLICATION NUMBER:  US/09/357,710A
; CURRENT FILING DATE:  1999-07-20
; PRIOR APPLICATION NUMBER:  US 08/838,682
; PRIOR FILING DATE:  1997-04-09
; PRIOR APPLICATION NUMBER:  US 60/016,976
; PRIOR FILING DATE:  1996-05-06
; PRIOR APPLICATION NUMBER:  US 60/022,125
; PRIOR FILING DATE:  1996-07-18
; NUMBER OF SEQ ID NOS:  21
; SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-357-710A-11

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	Query Match	100.0%;	Score 562;	DB 4;	Length 121;
	Best Local Similarity	100.0%;	Pred. No. 1.9e-50;		
	Matches 107;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	NIVMTQSPKSMMSVGRVTLTCKASENVNIVTVSWYQOKPEQSPKLLIYGASNRYTGVDP	60		
Db	7	NIVMTQSPKSMMSVGRVTLTCKASENVNIVTVSWYQOKPEQSPKLLIYGASNRYTGVDP	66		
Qy	61	RFTGSGSATDFTLTISVQAEDLADYHCGOGYSYPYTFGGGKTLEIK	107		
Db	67	RFTGSGSATDFTLTISVQAEDLADYHCGOGYSYPYTFGGGKTLEIK	113		

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RESULT      8
US-07-634-278-99
; Sequence 99, Application US/07634278
; Patent No. 5530101
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: CO, Man Sung
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: LANDOLFI, Nicholas F.
; APPLICANT: COELING, Kathleen L.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/634,278
; FILING DATE: 19-DEC-1990
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274

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; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975
; FILING DATE: 28-DEC-1988
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-002600
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 99:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 136 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-634-278-99

Query Match          92.7%; Score 521; DB 1; Length 136;
Best Local Similarity 91.6%; Pred. No. 3.3e+46;
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0

QY   1 NIVMTSPKSMVSGERVTLTKRASENVTVYSWYOKEPEQPKLLIYGASNRYTGVDP 60
      ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db   30 NIVMTSPKSMVTSGERTVTSKRASENVDTVYSWYOKEPEQPKLLIYGASNRYTGVDP 60
      ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

QY   61 RTFGGSATDFTLTSSVQAEDLADYHCGQGYSPYPFFGGGTGLEIK 107
      ||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||
Db   90 RTFGGSATDFTLTSSVQAEDLADYHCGQGSYNYPFFGSGTGLEIK 136
      ||||| :||||| :||||| :||||| :||||| :||||| :||||| :|||||

RESULT    9
US-08-477-728-99
; Sequence 99, Application US/08477728
; Patent No. 5585089
; GENERAL INFORMATION:
; APPLICANT: QUEEN, Cary L.
; APPLICANT: SCHNEIDER, William P.
; APPLICANT: SELICK, Harold E.
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
; NUMBER OF SEQUENCES: 113
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,728
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/634,278
; FILING DATE: 19-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/590,274
; FILING DATE: 28-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/310,252
; FILING DATE: 13-FEB-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/290,975

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; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 99:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 136 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-477-728-99

Query Match 92.7%; Score 521; DB 1; Length 136;  
Best Local Similarity 91.6%; Pred. No. 3.3e-46;  
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 NIVMTQSPKSMMSGVGVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRVTGVPD 60  
||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 30 NIVMTQSPKSMMSGVGVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRVTGVPD 89  
||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
  
QY 61 RTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGGKLEIK 107  
||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 90 RTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGGKLEIK 136

RESULT 10  
US-08-474-040-99  
; Sequence 99, Application US/08474040  
; Patent No. 5693761  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/474,040  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223

; REFERENCE/DOCKET NUMBER: 11823-002600  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 99:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 136 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-474-040-99

Query Match 92.7%; Score 521; DB 1; Length 136;  
Best Local Similarity 91.6%; Pred. No. 3.3e-46;  
Matches 98; Conservative 5; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 NIVMTQSPKSMMSGVGVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRVTGVPD 60  
||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 30 NIVMTQSPKSMMSGVGVTLTKKASENVVTVSVYQKPEQSPKLLIYGASNRVTGVPD 89  
||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
  
QY 61 RTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGGKLEIK 107  
||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 90 RTGSGSATDFTLTISVQAEDLADYHCGQGYSPYTFGGGKLEIK 136

RESULT 11  
US-08-487-200-99  
; Sequence 99, Application US/08487200  
; Patent No. 5693762  
; GENERAL INFORMATION:  
; APPLICANT: QUEEN, Cary L.  
; APPLICANT: CO, Man Sung  
; APPLICANT: SCHNEIDER, William P.  
; APPLICANT: LANDOLFI, Nicholas F.  
; APPLICANT: COELINGH, Kathleen L.  
; APPLICANT: SELICK, Harold E.  
; TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBLINS  
; NUMBER OF SEQUENCES: 113  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/487,200  
; FILING DATE: 7-JUN-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/634,278  
; FILING DATE: 19-DEC-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/590,274  
; FILING DATE: 28-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/310,252  
; FILING DATE: 13-FEB-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/290,975  
; FILING DATE: 28-DEC-1988  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-002610  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400

REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 11823-002600  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 99:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 136 amino acids

61 RFTGSGSATDFTLTISSVOAEDLADYHCGQGYSPYTFGGTKLEIK 107



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